

Search completed: August 25, 2004, 14:58:18
Job time : 1146.6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 5161.56 Seconds
(without alignments)
13086.780 Million cell updates/sec

Title: US-10-735-098-7

Perfect score: 2262

Sequence: 1 atgtgttaaacgaattatgg.....tcgaggaggtggaataatga 2262

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103.8	4.6	908	28	AZ548467
2	101.8	4.5	434	14	CA745444
3	100.8	4.5	263	13	BU005139
4	100.4	4.4	395	29	CE760553

C	5	100.4	4.4	843	28	AZ551618
C	6	100.2	4.4	232	29	CG321416
C	7	100.2	4.4	233	12	BJ454017
C	8	98.8	4.4	265	14	CA607797
C	9	98.8	4.4	880	28	AZ529191
10		98.6	4.4	264	13	BQ241566
11		98.6	4.4	332	14	CA566759
12		98.6	4.4	575	10	BF707975
13		98.4	4.4	960	28	CC143364
14		98.2	4.3	594	12	BM167059
15		98.2	4.3	612	28	BZ149404
16		98.2	4.3	739	28	BZ220379
17		98.2	4.3	799	28	BZ201507
18		98.2	4.3	1096	14	CK206118
19		97.6	4.3	605	28	BZ222147
20		97.6	4.3	665	13	BU432980
21		97.4	4.3	341	29	CS510654
22		97	4.3	278	13	BQ460618
23		97	4.3	617	14	CA743799
24		97	4.3	691	28	BH040136
25		97	4.3	890	28	BH146886
26		97	4.3	906	28	BH153606
27		96.6	4.3	531	14	CD913362
28		96.6	4.3	546	28	AZ600777
29		96.2	4.3	289	14	CA716220
30		96.2	4.3	340	13	BQ462203
31		96.2	4.3	471	12	BM166650
32		96.2	4.3	477	14	CD311846
33		96	4.2	622	13	BU418103
34		95.8	4.2	302	9	AA572217
35		95.4	4.2	311	14	CA699402
36		95.4	4.2	406	28	AZ509483
37		95.4	4.2	924	13	BQ925195
38		95.2	4.2	548	9	AI746770
39		95.2	4.2	675	28	BZ104011
40		95.2	4.2	3743	11	AK048184
41		94.4	4.2	537	14	CF380795
42		94.2	4.2	223	13	CA022136
43		94.2	4.2	866	28	AZ527885
44		94.2	4.2	877	28	AZ531291
45		94.2	4.2	912	28	AZ551092

ALIGNMENTS

RESULT 1
AZ548467
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ548467
ENTEK30TR Entamoeba histolytica Sheared DNA
genomic, genomic survey sequence.
908 bp
DNA linear
GSS 14-NOV-2000
Entamoeba histolytica

AZ548467.1 GI:11172102
GSS.
Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 908)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq primer: M13-Reverse
Class: shotgun

AZ551618 ENTVDV54TR
CG321416 CGYBI53TV
BJ454017 BJ454017
CA607797 wrl.pk008
AZ529191 ENTBV68TR
BQ241566 TAE05003E
CA566759 K0405E07-
BF707975 A634 LE A
CC143364 NDL32A13
BM167059 EST569582
BZ149404 CH230-395
BZ220379 CH230-312
BZ201507 CH230-445
CK206118 FGAS01769
BZ222147 CH230-361
BU432980 603221001
CES10654 tigr-gss-
BQ460618 HA06H01F
CA743799 wrl18.pk0
BH040136 RPT-24-2
BH146886 ENTPK48TF
BH153606 ENTPK48TF
CD913362 G550.1250
CA716220 HD02A2Dr
BM166650 EST569173
CD311846 StrPn691.
BU418103 603959413
AA572217 v151608.r
CA699402 wlk8.pk00
AZ509483 LM0352019
BQ925195 AGENCOURT
AI746770 ul07c01.y
BZ104011 CH230-227
AK048184 Mus muscu
CF380795 lac78f12.
CA022136 HZ42E07r
AZ527885 ENTPK479TR
AZ531291 ENTBQ34TR
AZ551092 ENTFFJ22TF

RESULT 3
BU0051139/c
LOCUS
DEFINITION QG7D20.Y9.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
BU0051139
ACCESSION QG7D20.Y9.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
VERSION BU0051139
KEYWORDS EST.
SOURCE BU0051139.1 GI:22439534
ORGANISM Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 263)
AUTHORS Koziak, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL http://comgenomics.ucdavis.edu/
COMMENT Unpublished (2002)
Contact: Alexander Koziak [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgpdb.ucdavis.edu/ for details.
Plate: QG7 row: D column: 20.

FEATURES
Location/Qualifiers
1..263
/organism="Lactuca sativa"
/mol_type="mRNA"
/culturvar="L.serriola"
/db_xref="taxon:4236"
/clone="QG7D20"
/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRCDNA5FIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_SEQ-Not found"

ORIGIN
Query Match 4.5%; Score 100.8; DB 13; Length 263;
Best Local Similarity 66.7%; Pred. No. 9.4e-10;
Matches 144; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 1391 AACCAAGCGCGAGATTAAGCGGAGGATGAAGAGGTTGCAGGGTGTATACGACGAAG 1450
DB 227 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 168
QY 1451 AAAGCGAAGACGAAGCCCTAGAACGACGACGCGCGAGAGACGAACTTCCGAGAGG 1510
DB 167 AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 108
QY 1511 ATATGCGAAGACGAAGACCAACCGCCGAGAGAGAAACCGAAGAGATTGATCAAGCG 1570
DB 107 AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 48
QY 1571 AAGAGGAGGAGTTGAGAACCCGACCAAGAAATTCG 1606
DB 47 AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGACCCCG 12

RESULT 4
CE760553
LOCUS
DEFINITION tigr-gss-dog-17000369997532 Dog Library Canis familiaris genomic, genomic survey sequence.
CE760553
ACCESSION CE760553.1 GI:37101172
VERSION
KEYWORDS GSS.
SOURCE
ORGANISM Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 395)
AUTHORS Kirkness, E.F., Bafna V., Halpern, A.L., Levy, S., Remington, K., Rusk, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

THE dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..395
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN
Query Match 4.4%; Score 100.4; DB 29; Length 395;
Best Local Similarity 63.0%; Pred. No. 1.2e-09;
Matches 155; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1391 AACCAAGCGCGAGATTAAGCGGAGGATGAAGAGGTTGCAGGGTGTATACGACGAAG 1450
DB 83 AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 142
QY 1451 AAAGCGAAGACGAAGCCCTAGAACGACGCGCGAGAGACGAACTTCCGAGAGG 1510
DB 143 AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 202
QY 1511 ATATGCGAAGACGAAGACCAACCGCCGAGAGAGAAACCGAAGAGTTGATCAAGCG 1570
DB 203 AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 262
QY 1571 AAGAGGAGGAGTTGAGAACCCGACCAAGAAATTCGCGGAGAGGCAACCGCGGTTGAG 1630
DB 263 AAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 322
QY 1631 GCAGCA 1636
DB 323 GAGGAA 328

RESULT 5
AZ551618/c
LOCUS
DEFINITION ENT54T8 Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
AZ551618
ACCESSION AZ551618
VERSION AZ551618.1 GI:11176919
KEYWORDS GSS.

SOURCE	Entamoeba histolytica
ORGANISM	Eukaryota; Entamoebidae; Entamoeba.
REFERENCE	1 (bases 1 to 843)
AUTHORS	Loftus,B., Van Aken,S. and Fraser,C.
TITLE	Determination of clone end sequences from Entamoeba histolytica
JOURNAL	HMI:IMSS sheared DNA library
COMMENT	Unpublished (2000) Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: bjloftus@tigr.org Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer:	M13-Reverse
Class:	Shotgun
High quality sequence start:	39
High quality sequence stop:	838.
FEATURES	Location/Qualifiers
source	1..843 /organism="Entamoeba histolytica" /mol_type="genomic DNA" /strain="HM1:IMSS" /db_xref="taxon:5759"
	/clone_lib="Entamoeba histolytica Sheared DNA" /note="Vector: pHOSt; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barell, Oxford University Press, 1999)."
ORIGIN	
Query Match	4.4%; Score 100.4; DB 28; Length 843;
Best Local Similarity	45.4%; Pred. No. 1.4e-09;
Matches 359; Conservative	0; Mismatches 431; Indels 0; Gaps 0;
QY	1396 AAGCGGGAAGAATAAGGGGAGATGAACGAGGTGCAGCGTTGATAACGACGAAGAAAGC 1455
DB	829 AAGAAGATTGATGATGAAGAAGATGATGATGAAGAAGATGATGATGAAGAAGATGAT 770
QY	1456 GAAGACGAAGCCGTAGAAGACCAAGCGCGGCGAAGAACGAAAACCTCCGAAGAGATTAAT 1515
DB	769 GAAGAAGATGATGAAGAAGAGAGTGATGATGAAGATGAAGATGATGAAGACGATGAAC 710
QY	1516 GC CGAAGACGAAGAAGCAACCGCCGAAGAAGAAACCGAAGAAGTTGATGAAGCCGAAG 1575
DB	709 GACGAATATGAATTAGAAGATGATGATGATGAAGAAGAAAGATGATGATGAAGATGAT 650
QY	1576 GAGGAAGTTGAGAACCCGAAGAAAATCCGCCGAGAGGCAACCGCGGTTCCAGCGAGC 1635
DB	649 GAAGACGATGAAGACGACGAANTATGAATTAGAAGATGATGATGAAGAAGAAAGAT 590
QY	1636 ATCTCGTCCTGACCAAGCCCTTAAGACGGCATATGATGATGAAGAGAGATGATGATGA 1695
DB	589 GATGATGAAGAGAGAGATGATGATGATGAAGATGATGATGAAGAAGAAAGAT 530
QY	1696 CGCACGGCAGAAACCGATATTCGCMACCGGAAACCGCCCATATACC GGACTTGGGA 1755
DB	529 GATGAAGAAGATGATGAAGATGATGATGAAGAAGAAAGATGATGATGAAGATGATGAA 470
QY	1756 GC CGCTATCGGCAACCCATTCATGGCAATCAGCGCGATGAAAAACGGCAAAGCA 1815

Db	469	GACGATGAAGACGACGAATATGAATTGAAGATGATGATGAAGAAGAAAGATGATGAT	410
QY	1816	GRAATTACCGTTGATTTCGACAAGAAATCGATTTCGGAAAGCTGACGAGCAAAACGGC	1877
Db	409	GAAGAAGAAGAAGATGATGATGAAGATGATGATGAAGAAGATGAAGATGATGATGAA	350
QY	1876	GTAGAACCCTGCTTTCCATATTTGAAGACGCGCAAGATTGATGGCAACGGTTTCCACGCGACA	1935
Db	349	GAAGAAGATGAAGATGATGATGAAGAAGAAGATGATGAAGAAGAAGATGAAGAAGAA	290
QY	1936	GCGCGCACTCGGAGAGCGGCATCATCTTTCCGGAATCGTTCCGACCGACCCCAAAACA	1995
Db	289	GAAGATGATCAAGAACAGATGATGAAGAAGAAGATGATGAAGAAGATGAAGATGAA	230
QY	1996	TTCCAGCTAGTAATCTTCGTGTAAGAGGAGGATTTCACGCCGCGCGCGGAATTG	2055
Db	229	TTAGAAGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGATGATGAAGAAGAA	170
QY	2056	GCGCGTACTATTTTCAATAATGATGGAAATCTTTAGTATTAACCTGAAATATTTGAAAT	2115
Db	169	GAAGATGATGATGATGATGAAGAAGAAGATGATGAAGAAGATGATGAAGAAGATGAAGAT	110
QY	2116	GAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGCTGAAGTTGAAGTTGAAGCTGAAGT	2175
Db	109	GATCAAGAAGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAAGATGATGAA	50
QY	2176	GGCAACAGT 2185	
Db	49	GACGACGAAT 40	
RESULT 6			
CG321416/c			
LOCUS	CG321416	232 bp	DNA linear GSS 26-AUG-2003
DEFINITION	OGYBI53TV ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMA0640J09,		
	genomic survey sequence.		
ACCESSION	CG321416		
VERSION	CG321416.1	GI:34238682	
KEYWORDS	GSS.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 232)		
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.		
TITLE	Consortium for Maize Genomics		
JOURNAL	Unpublished (2002)		
COMMENT	Other GSSs: OGYBI53TH Contact: Cathy Whitelaw		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA		
	Tel: 301-838-5843		
	Fax: 301-838-0208		
	Email: whitelawetigr.org		
	Seq primer: TF		
	Class: Sheared ends.		
FEATURES	Location/Qualifiers		
source	1..232 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBMA0640J09" /clone_lib="ZM 0.7_1.5_KB" /note="Vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"		
ORIGIN			
Query Match	4.4%; Score 100.2; DB 29; Length 232;		
Best Local Similarity	65.3%; Pred. No.1.2e-09;		

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Matches 147; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1391 AACCAAGCGGAGATTAAGGGGAGGATCAAGAGGTCAGCGCTTGATACGACGAAG 1450
Db 226 AAGAGAGAGAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
QY 1451 AAAGCGAAGACGAGCGCTAGAGACGAGCGCGGCGGAAGAGAGAGAGAGAGAG 1510
Db 166 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 107
QY 1511 ATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Db 106 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 47
QY 1571 AAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Db 46 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2

RESULT 7
BJ454017/c
LOCUS
DEFINITION
  BJ454017 K. Sato unpublished cDNA library, cv. Akashinriki
  vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
  baak45j15 5', mRNA sequence.
ACCESSION
  BJ454017
VERSION
  BJ454017.1 GI:21132592
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  ORGANISM
    Hordeum vulgare subsp. vulgare
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Poideae; Triticeae; Hordeum.
  1 (bases 1 to 233)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
FEATURES
  Location/Qualifiers
    1..233
      /organism="Hordeum vulgare subsp. vulgare"
      /mol_type="mRNA"
      /cultivar="Akashinriki"
      /sub_species="vulgare"
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      /clone="baak45j15"
      /tissue_type="leaves"
      /dev_stage="vegetative stage"
      /clone_lib="K. Sato unpublished cDNA library, cv.
      Akashinriki vegetative stage leaves"

ORIGIN
  Query Match 4.4%; Score 100.2; DB 12; Length 233;
  Best Local Similarity 65.3%; Pred. No. 1.2e-09;
  Matches 147; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1391 AACCAAGCGGAGATTAAGGGGAGGATCAAGAGGTCAGCGCTTGATACGACGAAG 1450
Db 228 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 169
QY 1451 AAAGCGAAGACGAGCGCTAGAGACGAGCGCGGCGGAAGAGAGAGAGAGAGAG 1510
Db 168 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 109
QY 1511 ATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Db 108 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 49

Matches 147; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1391 AACCAAGCGGAGATTAAGGGGAGGATCAAGAGGTCAGCGCTTGATACGACGAAG 1450
Db 226 AAGAGAGAGAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167
QY 1451 AAAGCGAAGACGAGCGCTAGAGACGAGCGCGGCGGAAGAGAGAGAGAGAGAG 1510
Db 166 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 107
QY 1511 ATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Db 106 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 47
QY 1571 AAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Db 46 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2

RESULT 8
CA607797/c
LOCUS
DEFINITION
  CA607797 265 bp mRNA linear EST 21-NOV-2002
  wrl.pk0082.f4 wrl Triticum aestivum cDNA clone wrl.pk0082.f4 5',
  end. mRNA sequence.
ACCESSION
  CA607797
VERSION
  CA607797.1 GI:25162959
KEYWORDS
  EST.
SOURCE
  Triticum aestivum (bread wheat)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Poideae; Triticeae; Triticum.
  1 (bases 1 to 265)
REFERENCE
  Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
  Miao, G., Caraher, N. and Hanafey, M.K.
  DuPont Wheat cDNA Sequence
  Unpublished (2002)
  Contact: Scott V. Tingey
  Crop Genetics
  E. I. DuPont de Nemours and Company
  1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
  Tel: 302-631-2602
  Fax: 302-631-2607
  Email: Scott.V.Tingey@USA.dupont.com
  Seq primer: M13.
FEATURES
  Location/Qualifiers
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      /organism="Triticum aestivum"
      /mol_type="mRNA"
      /db_xref="taxon:4565"
      /clone="wrl.pk0082.f4"
      /tissue_type="root"
      /clone_lib="wrl"
      /note="Vector: pbluescript SK+, Site.1: EcoRI; Site.2:
      XhoI; Wheat (Triticum aestivum L.) root; 7 day old
      seedling, light grown"

ORIGIN
  Query Match 4.4%; Score 98.8; DB 14; Length 265;
  Best Local Similarity 62.6%; Pred. No. 2.4e-09;
  Matches 142; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1389 TAAACCAAGCGGAGATTAAGGGGAGGATCAAGAGGTCAGCGCTTGATACGACGA 1448
Db 230 TGAAGNTGACGANGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 171
QY 1449 AGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1508
Db 170 AGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 111
QY 1509 GGAATATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1568
Db 110 AGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 51
QY 1569 CGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Db 50 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4

RESULT 9
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LOCUS
DEFINITION
  AZ529191 880 bp DNA linear GSS 03-NOV-2000
  ENTBTV68FR Entamoeba histolytica Sheared DNA Entamoeba histolytica
  genomic, genomic survey sequence.
ACCESSION
  AZ529191
VERSION
  AZ529191.1 GI:11081835

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JOURNAL COMMENT	DEFINITION
(Long) Unpublished (2001) Contact: Dawood B. Dawood	

DEFINITION	ACCESSION	ORGANISM
	VERSION	
	KEYWORDS	
	SOURCE	

REFERENCE AUTHORS	TITLE	JOURNAL COMMENT
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FEATURES
source

ORIGIN	Query Match	Best Local	Matches
Qw			12

151	157
Qy	Qy
Db	
151	157
Qy	Qy

RESULT 13	
CC143364	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	

REFERENCE AUTHORS TITLE JOURNAL	DATE	REMARKS
1. J. H.
2. J. H.
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99. J. H.
100. J. H.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT Other GSSs: NDL.32A13.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1. .594

/organism="Plasmodium yoelii yoelii"

/mol_type="mRNA"

/strain="17XL"

/sub_species="yoelii"

/db_xref="taxon:73239"

/clone="PYCOC02"

/dev_stage="Asexual blood stages"

/lab_host="E. coli XL-1 Blue"

/clone_lib="PYBS"

/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Pyl17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."

FEATURES

source

Location/Qualifiers

1. .960

/organism="Aedes aegypti"

/mol_type="genomic DNA"

/strain="liverpool"

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/clone="NDL.32A13"

/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

FEATURES

source

Location/Qualifiers

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Location/Qualifiers

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FEATURES

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Location/Qualifiers

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FEATURES

source

JOURNAL
COMMENT

Unpublished (1999)
 Other GSSs: CH230-395M1.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/oreringinformation.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 395 row: M column: 1
 Seq primer: SP6
 Class: BAC ends.
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 /mol_type="genomic DNA"
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 /db_xref="taxon:10116"
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 /sex="Female"
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 /clone_lib="CHORI-230 Segment 2"
 /notes="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
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 Pieter de Jong"

FEATURES

source

ORIGIN

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Query Match      4.3%; Score 98.2; DB 28; Length 612;
Best Local Similarity 64.1%; Pred. No. 3.6e-09;
Matches 148; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1395 AAAGCGGAAGATAAAGGGAGGATGAAGAGGGTGCAGCGCTTGATACGACGAGAGAG 1454
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QY 1455 CGAAGACGAGCCGTAGAGACGAGAGCGGCGGCGGAGAGACGAACTTCGAGAGAGATAA 1514
Db 217 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 276
QY 1515 TGGCGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1574
Db 277 GGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 336
QY 1575 GGAGGAGAGTGAAGAACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1625
Db 337 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387

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Search completed: August 25, 2004, 05:21:12
 Job time : 5163.56 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:53:30 ; Search time 7964.58 Seconds
(without alignments)
11558.757 Million cell updates/sec

Title: US-10-735-098-9

Perfect score: 2124

Sequence: 1 atgtgttaaccgaattatgg.....acaaggaggcaacacgatga 2124

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *

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2: gb_htg:*

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4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

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22: em_pl:*

23: em_ro:*

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28: em_fun:*

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32: em_ov:*

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41: em_in:*

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43: em_or:*

44: em_ov:*

45: em_ph:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	2124	100.0	2124	6	A98976
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11	1416	66.7	2519	1	AF072890
12	1375.4	64.8	9955	1	AE002504
13	1375.4	64.8	349980	6	AX044033
14	1296.2	61.0	2277	1	AF022781
15	1296.2	61.0	2277	6	A98968
16	1296.2	61.0	2277	6	BD074755
17	1296.2	61.0	5691	1	AF049349
18	1293	60.9	2537	1	AF031432
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22	497.6	23.4	1000	6	AX081510
23	497.6	23.4	1000	6	AX374691
24	231.8	10.9	3398	1	NMLBPAG
25	105.8	5.0	13297	10	AF317727
26	105.8	5.0	179685	10	AC122056
27	104.8	4.9	266939	2	AC098663
28	104.6	4.9	3300	6	AX685922
29	104.6	4.9	3300	6	AX685922
30	103.6	4.9	196963	2	AC110522
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34	103.2	4.9	194060	2	AC124191
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36	103	4.8	177128	2	AC112834
37	103	4.8	224469	10	AC113041
38	103	4.8	224843	2	AC140386
39	103	4.8	240033	2	AC147135
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41	102.8	4.8	171477	2	AC094726
42	102.6	4.8	173556	2	AC074388
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44	102.4	4.8	232224	2	AC110149
45	102.4	4.8	251960	2	AC107279

ALIGNMENTS

RESULT 1

AF123383

LOCUS

DEFINITION

Neisseria meningitidis strain 881607 lactoferrin-binding protein

precursor (lbpB) gene, complete cds.

ACCESSION

AF123383

VERSION

AF123383.1

KEYWORDS

SOURCE

ORGANISM

Neisseria meningitidis

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

1 (bases 1 to 2124)

Pettersson, A., van der Biezen, J., Joosten, V., Hendriksen, J. and

Tomassen, J.

2124 bp DNA linear BCT 24-MAY-1999

Pred. No. is the number of results predicted by chance to have a

TITLE Sequence variability of the meningococcal lactoferrin-binding protein LbpB
JOURNAL Gene 231 (1-2), 105-110 (1999)
MEDLINE 99250255
PUBMED 10231574
REFERENCE 2 (bases 1 to 2124)
AUTHORS Pattersen, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tomassen, J.
TITLE Direct Submissio
JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
FEATURES
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ORIGIN

Query Match 100.0%; Score 2124; DB 1; Length 2124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 9 from Patent WO9909176.
ACCESSION A98976
VERSION A98976.1 GI:6781936
KEYWORDS
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ORGANISM
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria
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Pettersson-Pernholm A. M. and Tommassen, J. P.
NEISSERIA LACTOFERRIN BINDING PROTEIN
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UNIV UTRECHT (NL); PETTERSSON FERNHOLM ANNIKA (NL)
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ORIGIN

Query Match 100.0%; Score 2124; DB 6; Length 2124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

BD074759

LOCUS

BD074759

DEFINITION

Neisseria lactoferrin-binding protein.

ACCESSION

BD074759

VERSION

1

KEYWORDS

JP 2001514894-A/5.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 2124)

AUTHORS

Feinholm, A.-M. and Thomsen, J. P. M.

TITLE

Neisseria lactoferrin-binding protein

JOURNAL

Patent: JP 2001514894-A 5 18-SEP-2001;

UNIVERSITY OF UTRECHT, TECHNOLOGY FOUNDATION

COMMENT

OS Unidentified

PN JP 2001514894-A/5

PD 18-SEP-2001

PF 10-AUG-1998

PR 15-AUG-1997

PT ANICA MARGARETA PETERSON FEINOLM, JOHANES PETRUS MARIA PI THOMSEN

PC C12N15/09, A61K39/095, A61K48/00, A61P31/12, C07K14/22, C07K16/12, C12N1/21, C12P21/02, C12P21/08, G01N33/15, G01N33/50, G01N33/68, PC C12N15/00

CC Strandedness: Double;

CC Topology: Linear;

CC Neisseria lactoferrin-binding protein

FT Key Location/Qualifiers

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FEATURES

source

100.0%; Score 2124; DB 6; Length 2124;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4	
AFI23382	
LOCUS	
DEFINITION	Neisseria meningitidis strain m981 linear BCT 24-MAY-1999 precursor (lbpB) gene, complete cds.
ACCESSION	AFI23382
VERSION	AFI23382.1 GI:4884690
KEYWORDS	.
SOURCE	Neisseria meningitidis
ORGANISM	Neisseria meningitidis
	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
	Neisseriaceae; Neisseria.
REFERENCE	1 (bases 1 to 2169)

AUTHORS Pettersson, A., van der Biezen, J., Joosten, V., Joosten, V., Hendriksen, J., and Tommaassen, J.

TITLE Sequence variability of the meningococcal lactoferrin-binding

JOURNAL protein lbpB

MEDLINE Gene 231 (1-2), 105-110 (1999)

PUBMED 99250255

REFERENCE 10231574

AUTHORS Pettersson, A., van der Biezen, J., Joosten, V., Joosten, V., Hendriksen, J., and Tommaassen, J.

TITLE Direct Submission

JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology,

FEATURES Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands

source Location/Qualifiers

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ORIGIN

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Best Local Similarity 84.5%; Pred. No. 0;
Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;

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QY	1081	ACAGCAACGATCAGATCAAAATCTGCGCTGCGCTCTGGAACACACACCAAAATCTTG	1140
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Db	1138	GATTTCTTAAAAATTTCCGTTGACAGGCAAGTGTGTGAAATCCCGACCGCTTTGAGGTT	1197
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QY	1534	GAACCTGAAGAAAGCTGAAGAGGAGAAACCCCGAAGAAATTTCCGCGGACGAAGAGGC	1593
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RESULT 6

BD074756

LOCUS

DEFINITION

Neisseria lactoferrin-binding protein.

ACCESSION

BD074756

VERSION

BD074756.1

KEYWORDS

JP 2001514894-A/2.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1. (bases 1 to 2169)

AUTHORS

Felholm, A.M.P. and Thomasen, J.P.M.

TITLE

Neisseria lactoferrin-binding protein

JOURNAL

Patent: JP 2001514894-A 2 18-SEP-2001.

COMMENT

UNIVERSITY OF UTRBCHT, TECHNOLOGY FOUNDATION

OS

Unidentified

PN

JP 2001514894-A/2

PD

18-SEP-2001

PF

10-AUG-1998

PR

15-AUG-1997

THOMASEN

ANICA MARGARETA PETERSON FELHOLM JOHANES PETRUS MARIA

PC

C12N15/09,A61K39/095,A61K39/395,A61K48/00,A61P31/12,C07K14/22,C07K16/12

PC

C12N1/21,C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/68,PC

C12N15/00

CC

Strandedness: Double;

CC

Topology: Linear;

PH

Key

Location/Qualifiers

FT

source

1. 2169

Location/Qualifiers

1. 2169

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FEATURES

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ORIGIN

Query Match

Best Local Similarity

Matches 1835;

Conservative

73.6%; Score 1562.4; DB 6; Length 2169;

84.5%; Pred. No. 0;

0; Mismatches 286; Indels 51; Gaps 5;

QY

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RESULT 7
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LOCUS Neisseria meningitidis serogroup A strain Z2491 complete genome;
DEFINITION segment 6/7.
ACCESSION NMA6Z2491
VERSION AL162757.2 GI:7380371
KEYWORDS
SOURCE
ORGANISM Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE
AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,
Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,
Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
Skelton,J., Whitehead,S., Spratt,B.G. and Barrall,B.G.
Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491
JOURNAL Nature 404 (6777), 502-506 (2000)
MEDLINE 20222556
PUBMED 10761919
REFERENCE
AUTHORS Parkhill,J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT
Notes:
Details of N. meningitidis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/N\_meningitidis/).
FEATURES
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fasta scores; E(): 0.96.7% identity in 183 aa overlap.
Contains Pfam match to entry PF00127 copper-bind, Copper
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QY 121 TTCAAGTCTAAGACGTTCCACTTCGCTTCGCGGGTCTTCGTTAGAAACACGCGCG 180
Db 18861 TTCAAGTCTAAGACGTTCCACTTCGCTTCGCGGGTCTTCGTTAGAAACACGCGCG 18802
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RESULT 8
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LOCUS
DEFINITION
Neisseria meningitidis strain H44/76 lactoferrin-binding protein precursor (lbpB) gene, complete cds.
ACCESSION
AF123380
VERSION
AF123380.1
KEYWORDS
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 2226)
Pettersson,A., van der Biesen,J., Joosten,V., Hendriksen,J. and Tommassen,J.
Sequence variability of the meningococcal lactoferrin-binding protein lbpB
Gene 231 (1-2), 105-110 (1999)
99250255
10231574
2 (bases 1 to 2226)
Pettersson,A., van der Biesen,J., Joosten,V., Hendriksen,J. and Tommassen,J.
Direct Submission
Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
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ORIGIN

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Best Local Similarity 83.3%; Pred. No. 7.6e-304;
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ORIGIN

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Query Match 70.6%; Score 1499.8; DB 6; Length 2226;
Best Local Similarity 83.3%; Pred. No. 7.6e-304;
Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;

QY 1 ATGTCTAAACCGAANTATGGGGCATTGCTTGTGTGCCCTTACTTTTGGCATCTTGTATC 60
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LOCUS
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(lbpB) gene, complete cds.
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VERSION
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RESULT 12

AE002504/c

LOCUS

DEFINITION

AE002504
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BCT 25-MAY-2000
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Thu Aug 26 10:18:19 2004

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REFERENCE	1 (bases 1 to 9955)		/db_xref="GI:7226787"
AUTHORS	Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C., Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D., Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blair,E., Clifton,H., Clark,E.B., Cotton,M.D., Utterback,T.R., Khouri,H., Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Massignani,V., Pizzi,M., Grandi,G., Sun,L., Smith,H.O., Fraser,C.M., Moxon,E.R., Rappuoli,R. and Venter,J.C.		/translation="MCKPNYGGIVLLPPLLASCIGNGFVQVVESTPTAYPTVTFKSK DVTPPPAGSSVETTPNRPVAVGAAMRLPRNTIASYKQDGTETIPDKHQAEEHLPLKKE DIILFDLTKEQADKLKKNERYSDVRVILTSKKEEKYQYQVFRAGYVFRABGKDN EKSTSDGKEFVNRFSDGVYVSGRPSQSLPSAGTVQYSGNWMYMDAKRHRTGKA VSTDLGYTTIYNEIGATSYEARDADDEKHPAEYIVFDNKTGLKGLKNQYVQNK SPNPEKPLTIYDITATLDGNRFTGSAKSTEVTKQHADKYLFFHTDADQRLGGF SGNPEKPLTIYDITATLDGNRFTGSAKSTEVTKQHADKYLFFHTDADQRLGGF SGNPEKPLTIYDITATLDGNRFTGSAKSTEVTKQHADKYLFFHTDADQRLGGF 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Query Match 64.8%; Score 1375.4; DB 1; Length 9955;
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Db	3945	GGCAACGTTTCTACGCGACACGACGCACTCGGAGAACGGCATCAATCTTTTCGGGAAAT	3886
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SOURCE	Neisseria meningitidis		
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
REFERENCE	1		
AUTHORS	Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C., Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M., Scarlato, V., Rappuoli, R., Frazer, C. M. and Grandi, G.		
TITLE	Neisseria genomic sequences and methods of their use		
JOURNAL	Patent: WO 0066791-A.112 09-NOV-2000;		
FEATURES	CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)		
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ORIGIN			
Query Match	64.8%;	Score 1375.4;	DB 6;
Best Local Similarity	80.2%;	Pred. No. 1.5e-277;	
Matches 1709;	Conservative	0;	Mismatches 371; Indels 51; Gaps 6;

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QY	121	TTCAAGTCTAGGAGCTTCCACATTCGCTCTCCGCGGTCTTCGCTAGAAACACGCGC	180
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VERSION AF022781.1 GI:2843172
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ORGANISM *Neisseria meningitidis*
Bacteria; *Proteobacteria*; *Betaproteobacteria*; *Neisseriales*; *Neisseriaceae*; *Neisseria*.
REFERENCE 1 (bases 1 to 2277)
AUTHORS Petersson, A., Prinz, T., Umar, A., van der Biesen, J. and Tommassen, J.
TITLE Molecular characterization of LbpB, the second lactoferrin-binding protein of *Neisseria meningitidis*
JOURNAL Mol. Microbiol. 27 (3), 599-610 (1998)
MEDLINE 98149315
PUBMED 9489671
REFERENCE 2 (bases 1 to 2277)
AUTHORS Petersson, A., Prinz, T., Umar, A., van der Biesen, J. and Tommassen, J.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-1997) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE

1 (bases 1 to 2277)

AUTHORS

Petersson-Fernholm, A.M. and Tommassen, J.P.

TITLE

NEISSERIA LACTOFERRIN BINDING PROTEIN

JOURNAL

Patent: WO 9809176-A 1 25-FEB-1999;

FEATURES

UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA MAR (NL)

source

location/Qualifiers

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ORIGIN

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Thu Aug 26 10:18:19 2004

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9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2124	100.0	2124	2	Aax23323 N. mening
2	1562.4	73.6	2169	2	Aax23320 N. mening
3	1516.8	71.4	2226	7	Aca41945 Prokaryot
4	1499.8	70.6	2226	2	Aax23321 N. mening
5	1375.4	64.8	110000	3	Continuation (2 of
6	1375.4	64.8	349980	3	Aaf21611 Neisseria
7	1296.2	61.0	2277	2	Aax23319 N. mening
8	1291.8	60.8	2262	2	Aax23322 N. mening
9	937.4	44.1	14652	3	Aaa81482 N. mening
10	497.6	23.4	1000	6	Aaf91389 N. mening
11	497.6	23.4	1000	6	Abk37769 DNA seque
12	428.8	20.2	707	3	Aaa81815 N. mening
13	104.6	4.9	3300	6	Abs67377 Neisseria
14	98.2	4.6	708	5	Aas69547 DNA encod
15	98.2	4.6	708	5	Aas75461
16	96.8	4.6	801	5	Aas90729 DNA encod
17	95.6	4.5	2334	5	Aas90705 DNA encod
18	95	4.5	400	5	Aas75460 DNA encod
19	95	4.5	963	5	Aas68580 DNA encod
20	94.4	4.4	49999	2	Aaz23896 Murine IO
21	94.4	4.4	49999	2	Aaz23891 Murine IO
22	94.2	4.4	453	5	Aas92079 DNA encod
23	93.8	4.4	248	5	Aas90707 DNA encod

C 24	93.8	4.4	305	4	AAI21797	Aai21797 Probe #11
C 25	93.8	4.4	305	4	ABA66871	Aba66871 Human foe
C 26	93.8	4.4	305	4	AAI47083	Aai47083 Probe #15
C 27	93.8	4.4	305	4	ABA48950	Aba48950 Human bre
C 28	93.8	4.4	305	4	ABA33942	Aba33942 Probe #12
C 29	93.8	4.4	305	4	AAK41027	Aak41027 Human bon
C 30	93.8	4.4	305	4	AAK15306	Aak15306 Human bon
C 31	93.8	4.4	305	4	ABS40624	Abs40624 Human liv
C 32	93.8	4.4	305	5	AAI07480	Aai07480 Probe #74
C 33	93.8	4.4	305	6	ABS15007	Abs15007 Human gen
C 34	93.8	4.4	483	5	AAS69549	Aas69549 DNA encod
C 35	93.8	4.4	496	4	AAI12609	Aai12609 Probe #25
C 36	93.8	4.4	496	4	ABA54309	Aba54309 Human foe
C 37	93.8	4.4	496	4	AAI33960	Aai33960 Probe #26
C 38	93.8	4.4	496	4	ABA43847	Aba43847 Human bre
C 39	93.8	4.4	496	4	ABA24068	Aba24068 Probe #25
C 40	93.8	4.4	496	4	AAK28026	Aak28026 Human bon
C 41	93.8	4.4	496	4	AAK02592	Aak02592 Human bra
C 42	93.8	4.4	496	4	ABS27626	Abs27626 Human liv
C 43	93.8	4.4	496	5	AAI02512	Aai02512 Probe #25
C 44	93.8	4.4	496	6	ABS02506	Abs02506 Human gen
C 45	93.2	4.4	390	5	AAS69541	Aas69541 DNA encod

ALIGNMENTS

RESULT 1
AAX23323
ID AAX23323 standard; cDNA; 2124 BP.
XX AC AAX23323;
XX DT 11-JUN-1999 (first entry)
XX DE N. meningitidis strain 881607 LbpB cDNA.

XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;
XX meningitis; diagnosis; treatment; ds.
XX OS Neisseria meningitidis.

XX FH Key Location/Qualifiers
XX CDS 1. .2124
XX FT /*tag= a
XX FT /product= "LbpB"
XX PN WO9909176-A1.

XX PD 25-FEB-1999.
XX PF 10-AUG-1998; 98WO-EF005117.
XX PR 15-AUG-1997; 97GB-00017423.
XX PR 05-FEB-1998; 98GB-00002544.
(UYUT-) RIJKSUNIV UTRECHT.
(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX PI Pettersson-Ferholm AM, Tommassen JPM;
XX DR WPI; 1999-190165/16.
XX DR P-PSDB; AAW93496.

XX PT New lactoferrin-binding protein B polynucleotides - obtained from
XX PT Neisseria meningitidis, used to develop products for the diagnosis,
XX PT prevention and treatment of neisserial disease, e.g. meningitis.

XX PS Claim 2; Page 105-109; 116pp; English.

XX CC This invention describes novel lactoferrin-binding protein B (LbpB)
XX CC strains of Neisseria meningitidis. The products of this invention can be
XX CC used for vaccinating humans against neisserial disease e.g. meningitis.

APP/CAIS

CC	Antibodies raised against the proteins of the invention can be used for									
CC	diagnosing or treating neisserial disease in humans. The LbpB									
CC	polypeptides can also be used for identifying compounds which inhibit the									
CC	polypeptides									
XX										
SQ	Sequence 2124 BP; 663 A; 461 C; 541 G; 459 T; 0 U; 0 Other;									
	Query Match	100.0%;	Score 2124;	DB 2;	Length 2124;					
	Best Local Similarity	100.0%;	Pred. No. 0;							
	Matches 2124;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
QY	1	ATGTGTAACCGAATTATGGCGCATTTGTTGGCTTACTTTTGGCATCTTGGCATC	60							
DB	1	ATGTGTAACCGAATTATGGCGCATTTGTTGGCTTACTTTTGGCATCTTGGCATC	60							
QY	61	GGCGGCAATTTCCGGCTGCAGCTGTTTCGAATCAACGCCGACCGGTACCCGCTCACT	120							
DB	61	GGCGGCAATTTCCGGCTGCAGCTGTTTCGAATCAACGCCGACCGGTACCCGCTCACT	120							
QY	121	TTCAGGTCTAAGGACGTTTCCCACTTCGCTCTCTCGCGGTCTTCGGTAGAAACACGCCG	180							
DB	121	TTCAGGTCTAAGGACGTTTCCCACTTCGCTCTCTCGCGGTCTTCGGTAGAAACACGCCG	180							
QY	181	GTCACACCGACCCGCGGTGGTGGCGGCAATCGCGCTGTGAGACGGAATATTGCAACTTCT	240							
DB	181	GTCACACCGACCCGCGGTGGTGGCGGCAATCGCGCTGTGAGACGGAATATTGCAACTTCT	240							
QY	241	GATAGAGATGGCAATGATTTTCCAAATAGCAAAACAAAGCAGAGAAAGCTGCTTTAAA	300							
DB	241	GATAGAGATGGCAATGATTTTCCAAATAGCAAAACAAAGCAGAGAAAGCTGCTTTAAA	300							
QY	301	GAGGAAGATATCCTGTTTTTATACGGTTTCCAAAAAGATCAACGTCAGCAGCTTAAAGAT	360							
DB	301	GAGGAAGATATCCTGTTTTTATACGGTTTCCAAAAAGATCAACGTCAGCAGCTTAAAGAT	360							
QY	361	AAAAATTCGTCAACCAATCTTACGGCAAGCATTACCAATCGGAAGAAAATAAAAA	420							
DB	361	AAAAATTCGTCAACCAATCTTACGGCAAGCATTACCAATCGGAAGAAAATAAAAA	420							
QY	421	TATGATTTATAATTTGTAGATGCAAGTTATGTTATATATACTAAAGACGGAAGAGATGAAAT	480							
DB	421	TATGATTTATAATTTGTAGATGCAAGTTATGTTATATATACTAAAGACGGAAGAGATGAAAT	480							
QY	481	GAGTGGACTTCAAAATTAACAAGCAGTCTACCAACCGGTTTGGTTATGACGGTTTGTATAT	540							
DB	481	GAGTGGACTTCAAAATTAACAAGCAGTCTACCAACCGGTTTGGTTATGACGGTTTGTATAT	540							
QY	541	TATTCGGAGAACATCTTTCGCAATCTTTACCGAGCGCGGAACGGTGAATATATCCGGC	600							
DB	541	TATTCGGAGAACATCTTTCGCAATCTTTACCGAGCGCGGAACGGTGAATATATCCGGC	600							
QY	601	AACCTGGCAATATATGACCGATGCCATAGTCATCGAACAGGAAAGCAGGAGATCTTAGC	660							
DB	601	AACCTGGCAATATATGACCGATGCCATAGTCATCGAACAGGAAAGCAGGAGATCTTAGC	660							
QY	661	GAAGATTGGGTTATATCGTTTATTTACGGTCAAAAATGTCGGAGCAACTTCTTATGCTGC	720							
DB	661	GAAGATTGGGTTATATCGTTTATTTACGGTCAAAAATGTCGGAGCAACTTCTTATGCTGC	720							
QY	721	ACTGCCGACGACCGGGAGGAAAAACATCTCGCAATATATACGGTTAATTTTCGACCAAAA	780							
DB	721	ACTGCCGACGACCGGGAGGAAAAACATCTCGCAATATATACGGTTAATTTTCGACCAAAA	780							
QY	781	ACTCTGAATGGCAGCTGATTAAAAATCAGTATGTGCAAAAGAGAGATGATCTTAAAAAA	840							
DB	781	ACTCTGAATGGCAGCTGATTAAAAATCAGTATGTGCAAAAGAGAGATGATCTTAAAAAA	840							
QY	841	CCACTGACCAATTTACGACATTAATGCAAAATTTGGACGGCAACCGCTTTACCGGAGTGCC	900							
DB	841	CCACTGACCAATTTACGACATTAATGCAAAATTTGGACGGCAACCGCTTTACCGGAGTGCC	900							
QY	901	AAAAGTTTAAACAGAGGTGAAGCAATCACGCTGATTAAGAAATATTTGTTTTTCCATACC	960							

Db	901	AAAAGTTTAAACACAGAGGTGAAGACGAATCACGCTGATAAAGAAATATTTGTTTTTCCATACC	960
Qy	961	GATGCCGATCAGCGGCTTGAGGGCGGTTTTTTTCGGCGATAGGGGGAAGAGCTTGCCGGA	1020
Db	961	GATGCCGATCAGCGGCTTGAGGGCGGTTTTTTTCGGCGATAGGGGGAAGAGCTTGCCGGA	1020
Qy	1021	CGGTTTTATCAGCAACGACAGCGTATTCGGCGTGTTCGAGGCAACAAAAACAGAG	1080
Db	1021	CGGTTTTATCAGCAACGACAGCGTATTCGGCGTGTTCGAGGCAACAAAAACAGAG	1080
Qy	1081	ACAGCAACGCAATCAGATACAAATCTTCCTGCGCTGCGGTAACACACCAAAATCTTG	1140
Db	1081	ACAGCAACGCAATCAGATACAAATCTTCCTGCGCTGCGGTAACACACCAAAATCTTG	1140
Qy	1141	GATTTCTTAAATTTTCCGTTGACGAGCAAGTGTGAAATATCCCGACCGTTTGAGGTT	1200
Db	1141	GATTTCTTAAATTTTCCGTTGACGAGCAAGTGTGAAATATCCCGACCGTTTGAGGTT	1200
Qy	1201	TCCACTATGCCCGATTTTGGTCAATCCCGACAAATCTTCTTGTGGAAGGCGTGAATTCCT	1260
Db	1201	TCCACTATGCCCGATTTTGGTCAATCCCGACAAATCTTCTTGTGGAAGGCGTGAATTCCT	1260
Qy	1261	TTGGTAACAAAGAACAAACCATCGATCTTCCGACGCGAGGAAATACCGTCCGTGCT	1320
Db	1261	TTGGTAACAAAGAACAAACCATCGATCTTCCGACGCGAGGAAATACCGTCCGTGCT	1320
Qy	1321	TGTTGCGACTTTTGGACCTATGTGAAATCTCGGACGATATAAAACCGACGCGCCGCTC	1380
Db	1321	TGTTGCGACTTTTGGACCTATGTGAAATCTCGGACGATATAAAACCGACGCGCCGCTC	1380
Qy	1381	CAACCGAAGGCGCAGGATGAAGAGGGGAGAGAGGGGTGTAGGGGTTGTATAACGGTAAA	1440
Db	1381	CAACCGAAGGCGCAGGATGAAGAGGGGAGAGAGGGGTGTAGGGGTTGTATAACGGTAAA	1440
Qy	1441	GAAAGCGAAGCAAAATCGGCGATGAAGAAACCAACGAGAACTTGAAGAGGAA	1500
Db	1441	GAAAGCGAAGCAAAATCGGCGATGAAGAAACCAACGAGAACTTGAAGAGGAA	1500
Qy	1501	GACGAAGATGAAGACGAAGAAATCGAAGAGAAACCTTGAAGAGAACTGAAGAGGAA	1560
Db	1501	GACGAAGATGAAGACGAAGAAATCGAAGAGAAACCTTGAAGAGAACTGAAGAGGAA	1560
Qy	1561	GAAACCGAAGAAATTTGCCGCGAGAAAGCAACGCGGTTTCAGGAGGATCTTCCGCC	1620
Db	1561	GAAACCGAAGAAATTTGCCGCGAGAAAGCAACGCGGTTTCAGGAGGATCTTCCGCC	1620
Qy	1621	ACTCCGAGAGCTTAAAGCGAGGACATCGACTTTTCTGAAAGGTATCCGACGGCG	1680
Db	1621	ACTCCGAGAGCTTAAAGCGAGGACATCGACTTTTCTGAAAGGTATCCGACGGCG	1680
Qy	1681	GAAAGCGCAATTTCCAAAAACCGAACCGGCAATTAACCGGCACTTTGGGAGGCGGTATC	1740
Db	1681	GAAAGCGCAATTTCCAAAAACCGAACCGGCAATTAACCGGCACTTTGGGAGGCGGTATC	1740
Qy	1741	GGCGTATCGGATAGTGTCCATTCAAAAGATAGCTATCGGATCAAGGGGCAAAA	1800
Db	1741	GGCGTATCGGATAGTGTCCATTCAAAAGATAGCTATCGGATCAAGGGGCAAAA	1800
Qy	1801	GCAGAAATTTACCGTTGATTTTGAAGCGAAGCGGTGTCCGGAATGTGTGAAGAAAAAAT	1860
Db	1801	GCAGAAATTTACCGTTGATTTTGAAGCGAAGCGGTGTCCGGAATGTGTGAAGAAAAAAT	1860
Qy	1861	GATACAAACCCCGCTTTTATATTGAAAAAGGTGTGATGACGGTAAACGGTTTCCAGCT	1920
Db	1861	GATACAAACCCCGCTTTTATATTGAAAAAGGTGTGATGACGGTAAACGGTTTCCAGCT	1920
Qy	1921	TTGGCGCATATCTGGGAGAACGGTATTGACTTTCTGGGAGGTTTGACTTAAACCGAAG	1980
Db	1921	TTGGCGCATATCTGGGAGAACGGTATTGACTTTCTGGGAGGTTTGACTTAAACCGAAG	1980
Qy	1981	AACCTTCAAGCGCAATCTTCTTGTAAACAGGCGGCTTTTATGGCCCGCAGCGCGAGAA	2040
Db	1981	AACCTTCAAGCGCAATCTTCTTGTAAACAGGCGGCTTTTATGGCCCGCAGCGCGAGAA	2040

QY 2041 TTGGCGGTATATATCGACAGCGACCGGAAATTCGTCGGGTATTTGGGCGGAAAAA 2100
Db |||||
2041 TTGGCGGTATATATCGACAGCGACCGGAAATTCGTCGGGTATTTGGGCGGAAAAA 2100
QY 2101 GATGACAAAGGAGGCAACACGATGA 2124
Db |||||
2101 GATGACAAAGGAGGCAACACGATGA 2124

RESULT 2

AAX23320

ID AAX23320 standard; cDNA; 2169 BP.

XX AC AAX23320;

XX 11-JUN-1999 (first entry)

XX N. meningitidis strain M981 LbpB cDNA.

XX LbpB; lactoferrin binding protein; vaccine; neisserial disease;

KW meningitis; diagnosis; treatment; ds.

XX Neisseria meningitidis.

XX Key

FH CDS

FT Location/Qualifiers

FT 1. 2169

FT /*tag= a

FT /product= "LbpB"

XX WO9909176-A1.

XX 25-FEB-1999.

XX 10-AUG-1998; 98WO-EP005117.

XX 15-AUG-1997; 97GB-00017423.

XX 05-FEB-1998; 98GB-00002544.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX (TECH-) TECHNOLOGY FOUND TSCHECHTING ST.

XX Pettersson-Fernholm AM, Tommassen JPM;

XX WPI; 1999-190165/16.

XX P-PSDB; AAW93493.

XX New lactoferrin-binding protein B polynucleotides - obtained from

XX Neisseria meningitidis, used to develop products for the diagnosis,

XX prevention and treatment of neisserial disease, e.g. meningitis.

XX Claim 2; Page 82-86; 116pp; English.

XX This invention describes novel lactoferrin-binding protein B (LbpB)

XX strains of Neisseria meningitidis. The products of this invention can be

XX used for vaccinating humans against neisserial disease e.g. meningitis.

XX Antibodies raised against the proteins of the invention can be used for

XX diagnosing or treating neisserial disease in humans. The LbpB

XX polypeptides can also be used for identifying compounds which inhibit the

XX polypeptides

XX Sequence 2169 BP; 675 A; 457 C; 550 G; 487 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 73.6%; Score 1562.4; DB 2; Length 2169;

XX Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;

QY 1 ATGTGTAACCGAATTATGCGGCATGTCCTGTCGCCCTTACTTTGGCATCTTCATC 60

Db |||||

1 ATGTGTAACCGAATTATGCGGCATGTCCTGTCGCCCTTACTTTGGCATCTTCATC 60

QY 61 GCGGCGAATTCGGGTGAGCGCTGTGTGGAATCAACCGCGACCGCGTACCCCGTCACT 120

Db |||||

1138 GATTCCTCTAAAAATTCGGTTCACGAGGCGACTGATGACCATCGCCGTAAGTTTGCATT 1197

Db 61 GCGGCGAATTCGGGTGAGCGCTGTGTGGAATCAACCGCGACCGCGTACCCGTCCTACT 120
QY 121 TTCAAGTCTAAGGAGCGTTCCCACTTCCCTCTCTCGCGGTCTTCGGTAGAAACACGCGC 180
Db |||||
121 TTCAAGTCTAAGGAGCGTTCCCACTTCCCTCTCTCGCGGTCTTCGGTAGAAACACGCGC 180
QY 181 GTCAACCGACCCCGCGTGTGGTGGGCAATCGCGCTGTGAGACGGAATATTGCACTTCT 240
Db |||||
181 GTCAACCGACCCCGCGTGTGGTGGGCAATCGCGCTGTGAGACGGAATATTGCACTTCT 240
QY 241 GATAAGGATGCGCAATGATTTTCCAAATAGCAAAACAGCAGAGAAAGCTGTCTGTTAAA 300
Db |||||
241 CGTGAAGATGCGCAGCGCAATTCCTCGATAGCAAAACAGCAGAGAAAGCTGTCTGTTAAA 300
QY 301 GAGGAAGATATCTCTGTTTATACGGTTCCTCAAAAGATCAACGTCAGCAGCTTAAAGAT 360
Db |||||
301 GAAGGTGATGTTCTGTTTATACGGTTCCTCAAAAGATCAACGTCAGCAGCTTAAAGAT 360
QY 361 AAAATTGTCACCAATCTTACCGCAAGCATTCACCATCGGAAAGAGATCAACGTCAGCAGCTTAAAGAT 420
Db |||||
361 GAAATTCATAAAGCTAATCTCGAGGCAAGCATTCACCATCGGAAAGATCAACGTCAGCAGCTTAAAGAT 420
QY 421 TATGATTATAAATTTGATAGTGAAGTATGATATATATATATATATATATATATATATAT 480
Db |||||
421 TATAATTATCGGTTTGTAGTCCGCTTATGTTTCTTAAATCGTTTATGAGCTATGACGCTTATATAT 480
QY 481 GAGTGGACTTCAAAATTCAGCAAGCATTCACCATCGGTTTGGTGTATGACGCTTGTGATAT 540
Db |||||
481 GAGAAAAATCATCGGATGAAAGCAGTTTCTTAAATCGTTTATGAGCTATGACGCTTGTGATAT 540
QY 541 TATTCGGGAGAACATCTTTCGCAATCTTACCGAGCGGGGAAACGCTGAAATATTCGCGC 600
Db |||||
541 TATCTCGGAGAACATCTTTCGCAATCTTACCGAGCGGGGAAACGCTGAAATATTCGCGC 600
QY 601 AACTGGCAATATATGACCGGATGCCATCGTCAATCGAGAGGTTAA---GGGGTTCCTCACT 657
Db |||||
601 AACTGGCAATATATGACCGGATGCCATCGTCAATCGAGAGGTTAA---GGGGTTCCTCACT 657
QY 661 GAAATTTGGCTTATATCGTTCCTTATATCGTCAATATCGTTCGAGAGCACTTCTTATCGTGG 720
Db |||||
658 GTGATTTGGGTATATACCATATATATGTTGTAATGAAATTCGGGCGAGCTTCTTATGAGCT 717
QY 721 ACTGCGAGCAGCGGAGGAGGAAACATCTCTCGCAATATATCGTTCCTTAAATTCGACCAAAA 780
Db |||||
718 AGCGATGCCGATGCCGGAAGAAACATCTCTCGCAATATATCGTTCCTTAAATTCGACCAAAA 777
QY 781 ACTCTGATGCGCAAGCTGATTAATAATGATGATGATGATGATGATGATGATGATGATGATG 840
Db |||||
778 AACCTGGAAGGTAAAGTTGATTAATAATGATGATGATGATGATGATGATGATGATGATGATG 837
QY 841 CCACTGACCAATTTACGACATTTACTGCAAAATTCGACCGGCAACCGCTTACCGGAGTGCC 900
Db |||||
838 CCACTGACCAATTTACGACATTTACGCAATTTACGCAATTTACGCAATTTACGCAATTTACG 897
QY 901 AAAGTTAAACAGAGGTGGAAGAGCAATCAAGCTGATTAAGAAATATTTGTTTTCATACC 960
Db |||||
898 AAAGTTAGCAACCGAGGTGGAAGAGCAATCAAGCTGATTAAGAAATATTTGTTTTCATACC 957
QY 961 GATGCGCATGAGCGCTTGGGCGGTTTTCGCGGATTAAGGGGGAAGAGCTTTCGCGGA 1020
Db |||||
958 GATGCGCATGAGCGCTTGGGCGGTTTTCGCGGATTAAGGGGGAAGAGCTTTCGCGGA 1017
QY 1021 CGGTTTATCAGCAACGACACGCGTATTTCCGCTGTTTCGAGGCAACCAAAAAACAGAG 1080
Db |||||
1018 CGGTTTATCAGTAAACGACACGCGTATTTCCGCTGTTTCGAGGCAACCAAAAAACAGAG 1077
QY 1081 ACAGCAACGCGATCAGATACAAATCTGCGCTGCGCTCTGGAAGAAACACACCAAAATCTTG 1140
Db |||||
1078 ACAGCAACGCGATCAGATACAAATCTGCGCTGCGCTCTGGAAGAAACACACCAAAATCTTG 1137
QY 1141 GATTCCTTAAAAATTTCCGTTGACGAGGCAAGTGTGAAATATCCCGACCGTTTGGAGTT 1200
Db |||||
1138 GATTCCTTAAAAATTTCCGTTGACGAGGCGACTGATGACCATCGCCGTAAGTTTGCATT 1197

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1201 TCACATATGCCGATTTTGGTTCATCCGCAAACTTTCTGTTCGAAGGGCGTGAATTCCT 1260
1198 TCACATATGCCGATTTTGGTTCATCCGCAAACTTTCTGTTCGAAGGGCGTGAATTCCT 1257
1261 TTGGTAAACAAAGCAAAACCATCATGATTCGCGACGGCAGGAAAATGACCGTCGCTGCT 1320
1258 TTGGTTAGCCAAAGAAACCATCGATTCGCCACGGCAGGAAAATGACCATCCGTCGCT 1317
1321 TGTTCGCACTTTTGGTTCATGTAACCTTCGCGACGGATTAACCAACCGCCCGCGCTC 1380
1318 TGTTCGCACTTTTGGTTCATGTAACCTTCGCGACGGATTAACCAACCGCCCGCGCTC 1377
1381 CAACCGAAGCGCGAGGATGAAGAGGGGACGAGAGGGGTGAGCGTTGATTAACGGTAAA 1440
1378 AAACCGAAGCGCGAGGATGAAGAGGGATTCGACATTCGATTAATGGCGAAGAAAGGAGAC 1437
1441 GAAA---GCGAAGACGAATCGCGATGAAGAGCACCAGGAG----- 1481
1438 GAAATTTCCGAAGATGATTAACGGCGAAGATGAAGTCAACGAAAGAGAGAGCTGAAGAA 1497
1482 --CGAAGTCGTAGAAGATGAAGACGAAGATGAAGACGAAGAAATCGAA-----GAA 1533
1498 ACCGAAAGAAACTGATGTAAGACCGAAGAGGAACCCGAAAGAACTGAAGAAACTGAA 1557
1534 GAACCTGAAGAGAGCTGAAGAGGAAGAAACCGCAAGAGAAATTCGCGCAGAGAGAGGC 1593
1558 GAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAA 1617
1594 AACGCGGTTCCGCGAGCATCTCCGCACTCCGCAAGCTCTAAAGCGAGGAGGACATCGAC 1653
1618 AACGCGGTTCCGCGAGCATCTCCGCACTCCGCAAGCTCTAAAGCGAGGAGGACATCGAC 1677
1654 CTTTTCCTGAAAGGATTCGCGACGGCGGAGCGACATTCGCAAAAACCGAAGCGGCGAT 1713
1678 CTTTTCCTGAAAGGATTCGCGACGGCGGAGCGACATTCGCAAAAACCGAAGCGGCG 1737
1714 TATACCGGCATTGGGAAGCGGTATCGCGTATCGGATA----- 1753
1738 TATACCGGCATTGGGAAGCGGTATCGCGTATCGGATAAGAAAGCGCAAGCTAGAT 1797
1754 -GTGGTACCTCCATTCAAAGGATAGCTATGCGAATCAAGGGGCAAAAGCAGAAATTACC 1812
1798 GGCACACTACGTCCATTCAAAGGATAGCTATGCGAATCAAGCGGCAAAAGCAGAAATTGAC 1857
1813 GTTGATTTGGAAGCAAGACGGTGTCCGGAATGCTGACAGAAAATAATGATCAACCCCC 1872
1858 GTTGATTTGTTGCGAAGTCGCTTCAGGTAACTGACAGAAAATAATGATCAACCCCC 1917
1873 GCTTTTATTAAGAAAGGTGATGATGACGGTAAAGGTTTCCAGCTTTGGCGCATACT 1932
1918 GCTTTTATTAAGAAAGGTGATGATGACGGTAAAGGTTTCCAGCTTTGGCGCATACT 1977
1933 CGGAGAACGGTATTCACCTTTCTGGGACGGTTTCGACTAACCCGCAAGAACTTCAAGCC 1992
1978 CGTGAATAAGGTGATGATTTGTTGGGCAAGGTTTCGACTTAATCCCAAGATTTTAAAGCC 2037
1993 GACAACTCTCTTGAACAGCGCGCTTTATGGCCCGCAGCGGCAAGATTTGGCGGTAAAT 2052
2038 AGTAACTCTCTGTAAGAGGAGGATTTATGGTCCGACGGCGGAGAGTTGGGTGTTAAAT 2097
2053 ATTATCAGACGCGCAAGAAATTCGTCGCGTATTTGGGCGGCAAAAGATGACAAAGGAG 2112
2098 ATTATCAGACGCGCAAGAAATTCGTCGCGTATTTGGTTCGCAAGAAAGATGATCAGGAG 2157
2113 GCAACACGATGA 2124
2158 GTGGAATAATGA 2169

RESULT 3
ACA41945
ID ACA41945 standard; DNA; 2226 BP.

ACA41945;
19-JUN-2003 (first entry)
Prokaryotic essential gene #23602.
Antisense; ds; prokaryotic essential gene; cell proliferation;
drug design; gene.
Neisseria meningitidis.
WO200277183-A2.
03-OCT-2002.
21-MAR-2002; 2002WO-US009107.
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
(ELIT-) ELITRA PHARM INC.
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
WPI; 2003-029926/02.
P-PSDB; ABU38075.
New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
Claim 14; SEQ ID NO 29815; 1766pp; English.
The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is one of the target
prokaryotic essential genes. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 2226 BP; 701 A; 466 C; 566 G; 493 T; 0 U; 0 Other;
Query Match 71.4%; Score 1516.8; DB 7; Length 2226;

Best Local Similarity	83.3%;	Pred. No. 0;	
Matches 1792;	Conservative	0; Mismatches	307;
			Indels
			51;
			Cons

QY	1	ATGTGTAACCGAATTATAGCGGCATGTCTGTGCGCTTACTTTTGGCATCTTGCATC	60
Db	1	ATGTGTAACCGAATTATGCGGCATGTCTGTGCGCTTACTTTTGGCATCTTGCATC	60
QY	61	GGCGGCAATTTCCGCGTGACGCTGTGTGCGAATCAACGCGACCGGTACCCCGTCAT	120
Db	61	GGCGGCAATTTCCGCGTGACGCTGTGTGCGAATCAACGCGACCGGTACCCCGTCAT	120
QY	121	TTCAAGTCTAAGACGCTTCCACTTCGCGCTCTCGCCGGGTCTTTCGGTAGAACAACGCGG	180
Db	121	TTCAAGTCTAAGACGCTTCCCACTTCGCGCCCTGCGCGGCTTCGGTAGAACAACGCGG	180
QY	181	GTCAACCGGACCGCGCTGTGTGGCGCAATGCGGCTGTTGAGACGGAAATTCGCAATCTT	240
Db	181	GTCAACCGGCGCGCGCTGTGTGGCGCAATGCGGCTGTTGAGGCGGAATATTGCTTTTCAT	240
QY	241	GATAAGGATGGCAATGATTTTCCAAATAGCAACAGACAGAGAAAGCTGTGCTTTAAA	300
Db	241	CGTGAAGATGGCAACGCAATTTCCGATAGCAACAGACAGAGAAAGCTGTGCTTTAAA	300
QY	301	GAGGAAGATATCCTGTGTTTTATACGGTTCCTCAAAAAAGATCAACGTCAGCAGCTTAAAGAT	360
Db	301	GAAGTGATGTCTGTGTTTTATACGGTTCCTCAAAAAAGATATACTTCAGCAGCTTAAGAT	360
QY	361	AAAAATTCGTAACCAAACTCTACGCGCAAGCATTAACATCGGAAAGAAAAATAAAAAA	420
Db	361	AAAAATTCACAGCGAACTCTAATGTAGAAATTAGGACATCAGAAAAATGAAAAATAAAAA	420
QY	421	TATGATTAATAATTTGTAGATCAGGTTATGTATATACTTAAGACGGTAATGTCGGTTTGTATAT	480
Db	421	TATGTTATGAATTTGTAGATCAGGTTATGTATATCTAAGAGGAAAAAGATGAAATTT	480
QY	481	GAGTGGACTTCAAAATTAACGACGCTTACCAACCGGTTTGTTATGACGGTTTGTATAT	540
Db	481	GAGTGGACTTCAAAATCAAAACGAGTTTACCTACCGGTTTGGTTATGACGGTTTGTATAT	540
QY	541	TATTCCGGGAGAACCTTTCCGCAATCTTTACGGAGCGGGGAAACGTTGAAATATTCGGC	600
Db	541	TATTCCGGGAGAACCTCTTCGCAATCTTTACCGAGCGGGGAAACGTTGAAATATTCGGC	600
QY	601	AATGGCAATATGACCGATGCCATAGCTCATCGAACAGAAAGACGAGAGATCCTAGC	660
Db	601	AATGGCAATATGACCGATGCCATAGCTCATCGAACAGAAAGACGAGATCCTAGC	660
QY	661	GAAATTTGGGTTATATCGTTTATTAACGTTCAAAATGTCCGACAACTTTATGCTGCG	720
Db	661	GAAATTTGGGTTATATCGTTTATTAACGTTCAAAATGTCCGAGCAACTTCTTATGCTGCG	720
QY	721	ACTCGCGACACCGGAGGGGAAAAATCTTCGCGAATATACGTTAATTTGACCAAAAAA	780
Db	721	ACTCGCGACACCGAGAGGGGAAACATCTTCGCGAATATACGTTAGATTTTCGGTAGAAA	780
QY	781	ACTCTGAATGGCAAGCTGATTAATAATCAGTATGTGCAAAAGACAGATGATCCTAAAAAA	840
Db	781	ACTTTGCGGGTAAATTAATTAATAATCAGTATGTGCAAAAGAAACCGATGAAAGAAA	840
QY	841	CCACTGACCAATTACGACATTTCTGCAAAATTTGACCGCAACCGCTTTTACCGCAGTGCC	900
Db	841	CCGCTGACCAATTTACGACATTTCTGCAACATTTGACCGCAACCGCTTTTACCGCAGTGCC	900
QY	901	AAAGTTAAACAGAGGTTGAAGACGAATTCAGCTGATAAAAGAAATATTGTTTTTCCATACC	960
Db	901	AAAGTTAAACCCGAGGTGAAGACGAATTCAGCTGATAAGAGCAATTTGTTTTTCCATACC	960
QY	961	GATGCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCGATAAGGGGGAAGAGCTTGCCGGA	1020
Db	961	GATGCCGATCAGAGGCTTGAGGGCGGTTTTTTCGGCGATAACGAGAGAGCTTGCCGGA	1020
QY	1021	CGGTTTATCAGCAACGACACACGCTATTCGGCGTTTCGAGGCGAAAAAAGAGAG	1080
Db			

181	Db	GTGCGCTCAACCGGGCCCTCGCTCGGTGGCGCAATCGCGCTGTTGAGCGGATTTTCGCA	240
235	QY	ACTCTGATAGAGTGGCAATGATTTTTCCAAATAGCAAAAACAACGAGAGAAAAGCTGTGCG	294
241	Db	ACTCTGATAGAGTTGGCAATGATTTTTCCAAATAGCAAAAACAACGAGAGAAAAGCTGTGCG	300
295	QY	TTTAAAGAGGAGATATCCTTGTTTTTATAGGTTTCCAAAAAAGATCAACGTCAGCAGCTT	354
301	Db	TTTAAAGAGGAGTATGTTCTGTTTTATACGGTTCAAAAAGATTAACCTTCAGTGCCTT	360
355	QY	AAAGATAAAATTCGTCAACCAAAATCTTACGGCAAGCAATTACCAATCGGAAAAAATAAT	414
361	Db	AAGGATAAATTCATCAACGCAATCCTAAATCTAGAAATTAGACATCAGAAAAATGAAT	420
415	QY	AAAAAATGATATAAAATTTGTAGATCAGGTTATGTATATATACTAAAGACGGAAAAAGAT	474
421	Db	AAAAAATATGTTATGAATTTGTGATCCCGTTATGTATATATACTAAAAAACGGAAACAGAT	480
475	QY	GAAATTTAGTGACTTTCAAATTTACAAGCAGTCTACCAACCGGTTTGGTTATGACGGTTTT	534
481	Db	GAAATTTAGTGACTTTCAAATTCGCAAGCAGTTTCTAATCGTTTTGGCTACGACGGTTTT	540
535	QY	GTATATTATTCGGAGAACATCCTTTCGCAATCTTTTACCGAGCGCGGAACGGTCGAATAT	594
541	Db	GTATATTATTCGGAGAACATCCTTTCCCAATCTTTTACCGAGCGCGGAACGGTCGAATAT	600
595	QY	TCCGCAACTGCGCAATATATGACCGATGCAATACGTCATCGAAACAGGAAAAACGAGAGAT	654
601	Db	TCCGTTAATTCGGCAATATATGACCGATGCAATACGTCATCGAAACAGGAAAAACGAGAGAT	660
655	QY	CCTAGCGAAGATTTGGGTTTATATCGTTTATTACGTTCAAATATGTCGAGAGCACTTCCTTAT	714
661	Db	CCTAGCGAAGATTTGGGTTTATCTCGTTTTATTACGGTCAAATATGTCGAGCAACTTCCTTAT	720
715	QY	GCTGGAATGCGACGACCGGAGGGAACACCTCGCGAATATACGGTTAAATTTTCGAC	774
721	Db	GCTGCGACTGCGACGACCGGAGGGAACACCTCGCGAATATACGGTTGAATTTGAT	780
775	QY	CAAAAACTCTGAATGGCAAGCTGATTAATAATTCAGTATGTGCAAAAAGAGAGATGATCCT	834
781	Db	AGAAAACTTTGACGGTCAATTAATTAATAATTCAGTATGTGCAAAAAGAAAAACCGATGAA	840
835	QY	AAAAAACCACTGACCAATTTACGACATTAATCGAAATTTGACGCAACCGCTTACCGCG	894
841	Db	AAGAAAACCACTGACCAATTTACGACATTTACGCAACATTTGACGCGCAACCGCTTACCGCG	900
895	QY	AGTGCCAAAGTTAAACAGAGGTGAAGCAATCAGCTGATAAAGAAATTTGTTTTTC	954
901	Db	AGTGCCAAAGTTAAACCGAGTTGAAGACGACCACTGATAAAGAGCATTTGTTTTTC	960
955	QY	CATACCGATGCCATCAGCGGCTTGAGGGCGTTTTTTCGGCGATGAAGGGGAGAGCTT	1014
961	Db	CATACCGATGCCATCAGCGGCTTGAGGGCGTTTTTTCGGCGATGAAGGGGAGAGCTT	1020
1015	QY	GCGGACGGTTTATCAGCAACGACACAGCGTATTCGGCGTGTTCGACGCAACAAAAA	1074
1021	Db	GCGGACGGTTTATCAGCAACGACACAGCGTATTCGGCGTATTCGACGCAACAAAAA	1077
1075	QY	ACAGAGACAGAAACCGCATCAGATACAAATCTCTGCCCTCGCTCGAAACACACACAAA	1134
1078	Db	ACAAACGATCAAAACGACGAGATACAAATCTCTGCTATGCGGCTCGAAAAACACACAAA	1137
1135	QY	ATCTTGATTTCTTAAAAATTTCCGTTGACGAGCGAGTGTGCAAAATCCCGACCGTTTT	1194
1138	Db	ATCTTGATTTCTTAAAAATTTCCGTTGACGAGCGAGCGGATTAATAATGCCGCCGTTTT	1197
1195	QY	GAGGTTTTCCATCTATGCCCGATTTTGGTTCATCCCGACAAACTTCTTGTGGAAGGGCGTGAA	1254
1198	Db	GCCATTTCCCTCTGCCCGATTTTGGCCATCCCGACAAACTCTCTTGTGGAAGGGCGTGAA	1257
1255	QY	ATTCCTTTTGTAAACAAAGAAACCAACCATGATCTTCGACGCGAGGAAAAATGACCGCTC	1314
1258	Db	ATTCCTTTTGTGTAGCAAGAAACCAACCATGAGCTTCGACGCGAGGAAAAATGACCGCTC	1317

1315 CGTCTGTTGGCACTTTTGGACCTATGTGAACCTCGACGGATATAAAACCGACGCC 1374
1318 CGTCTGTTGGCACTTTTGGACCTATGTGAACCTCGACGGATATAAAACCGACGCC 1377
1375 GCGCTCAACCGAAGCGCGAGATGAGAGAGGGGACGAAGAGGGTGTAGCGCTTGATAAC 1434
1378 GCAAGTAAACCAAGGCGGAGATGAGAGAGGGGATGAGAGGATGAGAGGATGAGAGG 1437
1435 GGTAAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1494
1438 GAGAGAGAGGCAACGGAAGATGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAG 1497
1495 GATGAAGAGCAAGATGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGG 1542
1498 GCGATGAGAGGAGGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAG 1557
1543 GAAGAGCTGAGAGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAG 1602
1558 GAAGCTGAGAGGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGG 1617
1603 TCAGGCGAGCATCTGCGCCACTCGGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAG 1662
1618 TCAGGCGGAGCATCTGCGCCACTCGGAGGCGGAGAGGCGGAGAGGCGGAGAGGCG 1677
1663 AAGGTATCCGACGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGG 1722
1678 AAGGTATCCGACGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCGGAGAGGCG 1737
1723 ACTTGGGAGCGGATCGGCGATCGGCGATCGGCGATCGGCGATCGGCGATCGGCGAT 1782
1738 ACTTGGGAGCGGATCGGCGATCGGCGATCGGCGATCGGCGATCGGCGATCGGCGAT 1782
1783 GCG---AATCAAGGGCGAAGAGCAGATTTACCGTTGATTTTCGAGCGAAGACCGTGTCC 1839
1783 GCGGATATAAAGCGGCGAAGAGCAGATTTACCGTTGATTTTCGAGCGAAGACCGTGTCC 1842
1840 GGAATGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1899
1843 GGAACGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1902
1900 GACGTTACGCTTTCACGCTTTTCGCGATATCGGAGAGAGAGAGAGAGAGAGAGAGAG 1959
1903 GAGGCGAATGTTTCCACGCGACAGCGCGCATCGGAGAGAGAGAGAGAGAGAGAGAGAG 1962
1960 CAGGTTTCGACTAACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2019
1963 AATGATTCGACTAATCTCCAGGTTTCAAGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 2022
2020 TATGGCCCGCAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2079
2023 TACGGCCCGCAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2082
2080 GCGGATTTGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2114
2083 GGTATAACTGAGATATCTGAAATGAGCTGAGAGC 2117

RESULT 5
AA81489_1/c
Continuation (2 of 9) of AA81489 from base 100001 (N. meningitidis partial DNA sequence
WP Sequence split into 9 fragments LOCUS AA81489 Accession AA81489
WP Fragment Name Begin End
WP AA81489_0 1 110000
WP AA81489_1 100001 210000
WP AA81489_2 200001 310000
WP AA81489_3 300001 410000
WP AA81489_4 400001 510000
WP AA81489_5 500001 610000
WP AA81489_6 600001 710000
WP AA81489_7 700001 810000
WP AA81489_8 800001 837096

Query Match 64.8%; Score 1375.4; DB 3; Length 110000;
Best Local Similarity 80.2%; Pred. No. 0;
Matches 1709; Conservative 0; Mismatches 371; Indels 51; Gaps 6;
QY 1 ATGTGTAACCGGAATTTATGGCGCATTTGCTTGTGCTTACTTTTGGCATCTTGTATC 60
Db 64252 ATGTGTAACCGGAATTTATGGCGCATTTGCTTGTGCTTACTTTTGGCATCTTGTATC 64193
QY 61 GCGGCAATTTGCGGCTGCGAGCTGTTTGCATCAACGCGGACCGGTCACCGTCAC 120
Db 64192 GCGGCAATTTGCGGCTGCGAGCTGTTTGCATCAACGCGGACCGGTCACCGTCAC 64133
QY 121 TTCAAGTCTAAGAGAGCTTCCCACTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 180
Db 64132 TTCAAGTCTAAGAGAGCTTCCCACTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCC 64073
QY 181 GTCAACCGAGCCCGCTTGGTTCGCGCAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 240
Db 64072 GTCAACCGAGCCCGCTTGGTTCGCGCAATTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 64013
QY 241 GATAAGGATGCAATGATTTTCCAAATAGCAACAGCAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 64012 AAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 63953
QY 301 GAGGAGAGATATCTTCTTTTATACGGTTTCCAAAGAGATCAACGTCAGCAGCTTAAAGAT 360
Db 63952 GAGGAGAGATATCTTCTTTTATACGGTTTCCAAAGAGATCAACGTCAGCAGCTTAAAGAT 63893
QY 361 AAAATTCGTAACCAATCTTACGCAAGCATTCACATCGGAGAGAGAGAGAGAGAGAGAGAG 420
Db 63892 AAAATTCGTAACCAATCTTACGCAAGCATTCACATCGGAGAGAGAGAGAGAGAGAGAGAG 63833
QY 421 TATGATTAATATTTGTAGATGCAAGTTATGTAATATCTA-----AAGCAGAGAGAGAT 474
Db 63832 TATGATTAATATTTGTAGATGCAAGTTATGTAATATCTA-----AAGCAGAGAGAGAT 63773
QY 475 GAAATTCAGTGGCATCTTCAATTTACAGCAGCTTACCAACCGGTTTGTATGACGTTT 534
Db 63772 GAAATTCAGTGGCATCTTCAATTTACAGCAGCTTACCAACCGGTTTGTATGACGTTT 63713
QY 535 GTATATTTATTCGAGAGAGATCTTTCGCAATCTTTCAGCGCGGAGAGAGAGAGAGAGAT 594
Db 63712 GTATATTTATTCGAGAGAGATCTTTCGCAATCTTTCAGCGCGGAGAGAGAGAGAGAT 63653
QY 595 TCGGCAACCTGCAATATATGACGATGCAATGATGATGATGATGATGATGATGATGATGAT 654
Db 63652 TCGGCAACCTGCAATATATGACGATGCAATGATGATGATGATGATGATGATGATGAT 63596
QY 655 CCTAGCGAAGATTTGGGTTATATCGTTTATTTACGTCGCAATCTTTCAGCGAGCACTTCTAT 714
Db 63595 CCTAGCGAAGATTTGGGTTATATCGTTTATTTACGTCGCAATCTTTCAGCGAGCACTTCTAT 714
QY 715 GCTGCGATCTGCGACGACCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
Db 63535 GAGGCTAGGAGATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 63476
QY 775 CAAAAAATCTGAAATGCGAGCTGATTTAAATCAGTATGTGCAAAAGAGAGAGAGAGAGAGAG 825
Db 63475 CAAAAAATCTGAAATGCGAGCTGATTTAAATCAGTATGTGCAAAATGAAATGAAATGAAAT 63416
QY 826 GATGATCTTAAAAACCACTGACCATTTTACGACATTTTACGACATTTTACGACATTTTACG 885
Db 63415 AATGAGCCCAAAACCGCTGACCATTTTACGACATTTTACGACATTTTACGACATTTTACG 63356
QY 886 TTTACCGGAGTGCAGAGTTTAAACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 945
Db 63355 TTTACCGGAGTGCAGAGTTTAAACAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 63296
QY 946 TTGTTTTTCCATACCGATGCGGATGAGGCGGTTGAGGCGGTTTTCGCGGATGAGGCGG 1005
Db 63295 TTGTTTTTCCATACCGATGCGGATGAGGCGGTTGAGGCGGTTTTCGCGGATGAGGCGG 63236
QY 1006 GAAGAGCTTGGCGAGCGGTTTATCAGCAACGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1065

Db	99481	ATGTGTAAACCGAATATATGGCGGCAATGTCTTGTGGCCCTTACTTTTAGCATCTTGTATC	99422
Qy	61	GGCGCAATTTTCGGCGTGACCCCTGTTGTTCGAATCAACGCGGACCGGTACCCCGTCACT	120
Db	99421	GGCGCAATTTTCGGCGTGACCCCTGTTGTTCGAATCAACGCGGACCGGTACCCCGTCACT	99362
Qy	121	TTCAAGTCTAAGAGAGTTTCCCACTTCCTCCCTCTCCCTGCTTCCGCTAGAAACCAACGCGG	180
Db	99361	TTCAAAATCTAAGAGAGTTTCCCACTTCCTCCCTCTCCCTGCTTCCGCTAGAAACCAACGCGG	99302
Qy	181	GTCAACCGACCCCGGTTGGTGGGCAATTCGGCTGTTGTGAGACGGAATATTGCAACTTCT	240
Db	99301	GTCAACCGACCCCGGTTGGTGGGCAATTCGGCTGTTGTGAGACGGAATATTGCAACTTCT	99242
Qy	241	GATPAGGATGGCAATGATTTTCCAAATAGCAAAACAGCAGCAAGAAAGCTGCTTAA	300
Db	99241	AAACAAGACGTACGGAAATTCGCAACAGATCAGCAGAGGAGATCTGCCGCTTAA	99182
Qy	301	GAGGAAGATATCTCTGTTTATACGGTTCCAAAAAGATCAACGTCAAGAGCTTAAAGAT	360
Db	99181	GAGGAAGATATCTCTGTTTATAGACGGTACGCTGAAGAGACAGGCTGACAACTTAAAAAG	99122
Qy	361	AAAAATTCGTCACCAAACTCTACGGCAAGATTTACCAATCGGAAAGAAATATAAAAA	420
Db	99121	AAAAATTCGTCACCAAACTCTGATGTGAGGGTTATCAATCGAATAAAGAAAGAAAA	99062
Qy	421	TATGATTAATAATTTGTAGATGAGGTTATGTATATACATA	474
Db	99061	TATCAATATCAATTTGTCGTCGGGCTATGTGTTTACAGGGCGGAAGAAAGATAT	99002
Qy	475	GAAATGTAGTGACTTCAAAATPACAGCAAGTCTACCAACCGGTTTGGTTATCACCGGTTTT	534
Db	99001	GAATAAGAAAGAACTTCTGATGGTAAGGAGTTTGTAAACCGATTTAGTTATACCGTTTT	98942
Qy	535	GTATATTTATTCGGAGAACATCTTTCGCAATCTTTACGAGCGCGGAAACGTTGAAATAT	594
Db	98941	GTATATTTATTCGGAGAACATCTTTCGCAATCTTTACGAGCGCGGAAACGTTGAAATAT	98882
Qy	595	TCCGCAACTGGCAATATATGACCATGCTATACGTCATCGAAGCAAGGAGAGAT	654
Db	98881	TCCGTAATGGCAATATATGACCATGCTATACGTCATCGAAGCAAGGAGAGAT	98825
Qy	655	CTAGCGAAGATTTGGGTTATATGTTTATACGGTCAAAATGTCCGAGCAACTTCTTAT	714
Db	98824	TCCAGTACGATTTGGGTTATATACCAATATTTATGTAATGAAATTTGGGCACTTCTTAT	98765
Qy	715	GCTCGACTCGGACGACCGGAGGAAACATCTGCGCAATATACGGTTAAATTTGAC	774
Db	98764	GAGCTAGGATGCGGACGACGAGGAAAGCATCTGCGCAATATACGGTTAAATTTGAT	98705
Qy	775	CAAAAACTCTGATGGCAAGCTGATTAATAATCAGTATGTGCAAAAGA	825
Db	98704	AACAAAACCCTGAATGCAAGCTGATTAATAATCAGTATGTGCAAAATAAAGTAATCCA	98645
Qy	826	GATGATCTTAAAAACCACTGACATTTACGATTAACGATTAACGATTAACGATTAACGAT	885
Db	98644	AATGAGCCCAAAAAACCGCTGACATTTACGATTAACGATTAACGATTAACGATTAACGAT	98585
Qy	886	TTTACCGGAGTCCCAAGTTTACAGAGGTGAAGCAAGATCAACGCTGATAAAGATAT	945
Db	98584	TTTACCGGAGTCCCAAGTTTACAGAGGTGAAGCAAGATCAACGCTGATAAAGATAT	98525
Qy	946	TTGTTTTTCCATACCGATCCGATCAGCGCTTGTAGGGCGGTTTTTTCGCGATAGAGGG	1005
Db	98524	TTGTTTTTCCATACCGATCCGATCAGCGCTTGTAGGGCGGTTTTTTCGCGATAGAGGG	98465
Qy	1006	GAAAGCTTTCGCGAGCGTTTATPAGCAACGACAGCGGATTTTCGCGGTTTCGAGGC	1065
Db	98464	GAAAGCTTTCGCGAGCGTTTATPAGCAACGACAGCGGATTTTCGCGGTTTCGAGGC	98405
Qy	1066	AAACAAAAACAGACAGCAACGATCAGATACAAATCTCTGCCCTGCTCGAAAA	1125
Db	98404	AAACAAAAACAGACAGCAACGATCAGATACAAATCTCTGCCCTGCTCGAAAA	98345

Qy	1126	CACACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGAGGCAAGTGTGTGAAAAATCCC	1185
Db	98344	CACACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGAGGCAAGTGTGTGAAAAATCCC	98285
Qy	1186	CGACCGTTTGAAGTTTCCACTATGTCGCCGATTTTGGTCAATCCGACAAACTCTCTGTGCGAA	1245
Db	98284	CGTGAGTTTGCATTTCTCTATGTCGCCGATTTTGGTCAATCCGACAAACTCTCTGTGCGAA	98225
Qy	1246	GGCGGTGAATTTCTTTGGTAAACAAAGAAACCAATCGATCTTCCGACGCGCAGGAAA	1305
Db	98224	GGCGGTGAATTTCTTTGGTAAACAAAGAAACCAATCGATCTTCCGACGCGCAGGAAA	98165
Qy	1306	ATGACCGTTCGTTGTTTGGGACTTTTGGACCTATGTGAACTCGGACGGATPAAAAACC	1365
Db	98164	ACGACATTCGAACTTCTGCGGATTTTCTGACCTATGTGAACTCGGACGGATPAAAAACC	98105
Qy	1366	GAAACGCGCCGCTCCAAACCGAGGCGCAGGATGAAGAGGGGACGAAAGAGGCTGTAGGC	1425
Db	98104	GAAACGCGCCGCTCCAAACCGAGGCGCAGGATGAAGAGGGGACGAAAGAGGCTGTAGGC	98045
Qy	1426	GTGTAAACGTTAAGAAAGCGAAGACGAAATCGGCGATGAAGAAACACCGGAGACGAA	1485
Db	98044	GTGTAAACGTTAAGAAAGCGAAGACGAAATCGGCGATGAAGAAACACCGGAGACGAA	97985
Qy	1486	GTCTAGAAAGATGAAGACGAAGATGAAGAGGAGGAGAAATCGAAGAGAACCTGAAGAA	1545
Db	97984	GCCGTAAAGACGAAGGACGAAAGACGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	97940
Qy	1546	GAACTGAAGAGGAAACCCGAAAGAAATTTGCCGCAAGAAAGGAGGAGGAGGAGGAGGAGG	1605
Db	97939	GAACTGAAGAGGAAACCCGAAAGAAATTTGCCGCAAGAAAGGAGGAGGAGGAGGAGGAGG	97880
Qy	1606	GCGAGCATCTCTCCCACTCTCCGAGAGCTCTTAAAGCAGGACATCGACCTTTTCTCGAAA	1665
Db	97879	GACGAGCATCTCTCCCACTCTCCGAGAGCTCTTAAAGCAGGACATCGACCTTTTCTCGAAA	97820
Qy	1666	GGTATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1725
Db	97819	GGTATCCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	97760
Qy	1726	TGGGAAGCGGTATCGGCGTATCGGATAGTGTGCTAGCTCCATTCAAAAGGAGTAGCTATCGG	1785
Db	97759	TGGGAAGCGGTATCGGCGTATCGGATAGTGTGCTAGCTCCATTCAAAAGGAGTAGCTATCGG	97715
Qy	1786	---AATCAAGGGCAAAAGCAGATTTACGTTGATTTGGAAGGAGAGAGCGGTGTCCGGA	1842
Db	97714	GATTAAGAGCGGCAAAAGCAGATTTACGTTGATTTGGAAGGAGAGAGCGGTGTCCGGA	97655
Qy	1843	ATGCTGACAGAAAAAATGATACAAACCCCGCTTTTATTTATTTGAAAAAGGTGTGATTGAC	1902
Db	97654	ACGCTGACAGGAGGAAACGCTGTAGAACCTGTCTTCATATTGAAAAAGGAGGAGGAGGAGG	97595
Qy	1903	GGTAAACGTTTCCGCTTTGGCGCATATCTGGGAGAACGGTATTTGACCTTTCTTGGGCGAG	1962
Db	97594	GGTAAACGTTTCCGCTTTGGCGCATATCTGGGAGAACGGTATTTGACCTTTCTTGGGCGAG	97535
Qy	1963	GGTTCGACTAACCCGAGAGAACTTCAAGCGGACAAATCTTCTTGTAAACAGCGGCTTTTAT	2022
Db	97534	GGTTCGACTAACCCGAGAGAACTTCAAGCGGACAAATCTTCTTGTAAACAGCGGCTTTTAT	97475
Qy	2023	GGCCCGCAGCGCGAGAAATGGGCGGTAATATATGACAGCGACCGGAAATTCGGTGGC	2082
Db	97474	GGCCCGCAGCGCGAGAAATGGGCGGTAATATATGACAGCGACCGGAAATTCGGTGGC	97415
Qy	2083	GTATTTGGGCGCAAAAAAGATGACAGGAGG	2113
Db	97414	ATAACTGAAGTACTGAAAAATAAGTTGATG	97384

RESULT 7
AX23319
ID AX23319 standard; cDNA; 2277 Bp.

Thu Aug 26 10:18:19 2004

XX AC AAX23319;
XX DT 11-JUN-1999 (first entry)
XX DE N. meningitidis strain BNCV LbpB cDNA.
XX KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
XX KW meningitis; diagnosis; treatment; ds.
XX OS Neisseria meningitidis.
XX FT Key Location/Qualifiers
XX FT CDS 100..2277
XX FT /*tag= a
XX FT /product= "LbpB"
XX WO9909176-A1.
XX 25-FEB-1999.
XX 10-AUG-1998; 98WO-EP005117.
XX 15-AUG-1997; 97GB-00017423.
XX 05-FEB-1998; 98GB-00002544.
XX (UYUT-) RIJKSUNIV UTRECHT.
XX PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING St.
XX XX Pettersson-Fernholm AM, Tommassen JPM;
XX PI WPI; 1999-190165/16.
XX DR P-PSDB; AAW93492.
XX XX New lactoferrin-binding protein B polynucleotides - obtained from
XX PT Neisseria meningitidis, used to develop products for the diagnosis,
XX PT prevention and treatment of neisserial disease, e.g. meningitis.
XX PS Claim 2; Page 74-78; 116pp; English.
XX CC This invention describes novel lactoferrin-binding protein B (LbpB)
XX CC strains of Neisseria meningitidis. The products of this invention can be
XX CC used for vaccinating humans against neisserial disease e.g. meningitis.
XX CC Antibodies raised against the proteins of the invention can be used for
XX CC diagnosing or treating neisserial disease in humans. The LbpB
XX CC polypeptides can also be used for identifying compounds which inhibit the
XX CC polypeptides
SQ Sequence 2277 BP; 700 A; 469 C; 573 G; 535 T; 0 U; 0 Other;
Query Match 61.0%; Score 1296.2; DB 2; Length 2277;
Best Local Similarity 79.0%; Pred. No. 5.7e-312;
Matches 1672; Conservative 0; Mismatches 373; Indels 72; Gaps 8;
QY 1 ATGTGTAACCGAATTATGCGCGCATGTCTGTGCGCTTACTTTTGGCATCTTGATC 60
DB 100 ATGTGTAACCGAATTATGCGCGCATGTCTGTGCGCTTACTTTTGGCATCTTGATC 159
QY 61 GCGCGCAATTTCGCGGTGACGCTGTGTGCAATCAACGCGACCGCGTACCCCGTCAC 120
DB 160 GCGCGCAATTTCGCGGTGACGCTGTGTGCAATCAACGCGACCGCGTACCCCGTCAC 219
QY 121 TTCAAGTCTAAGACGTTCCCACTTCGCTCCGCGGTCTTCGGTAGAACAACGCGCG 180
DB 220 TTCAAGTCTAAGACGTTCCCACTTCGCTCCGCGGTCTTCGGTAGAACAACGCGCG 279
QY 181 GTCACCGACCGCGGTGTGCGGCAATGCGGTGTGTGACACCGAATATTGCAACTTCT 240
DB 280 GTCACCGCGCGCGGTGTGCGGCAATGCGGTGTGTGACACCGAATATTGCAACTTCT 339
QY 241 GATAGAGTGGCAATGATTTTCCAAATAGCAAAACAAGCAGAGAAAGAGCTGCTGTTAAA 300
DB 340 CGTGAGATGGCAGGAATTCCTAATAGCAAAACAAGCAGAGAAAGAGCTGCTGTTAAA 399

301 GAGCAAGATATCTCTGTTTATACGGTTCACAAAGAGATCAACGTCAGCAGCTTAAAGAT 360
DB |||||
400 GAAGGTGATGTTCTGTTTATACGGTTCACAAAGAGAAATAAATTCACCAACTTAAAGC 459
QY |||||
361 AAAATTGTCACCAAAATCTACGGCAGCATTTACACATCGGAAGAAAGAAATAAAAAA 420
DB |||||
460 GAAATTCATAAAGCTGATTCGGATGTAGAAATTAGGACATCAGAAAAGGAAATAAAAAA 519
QY |||||
421 TATGATTATAAATTTAGATGCGAGTTATGTATATATAAAGACGGAAGAGATGAAT 480
DB |||||
520 TATGATTATAAATTTAGATGCGAGTTATGTATA---TGTAAGGGAAGAGATGAAT 576
QY |||||
481 GAGTGGACTTCAAAATTACAAGCAGTCTACCAACCGGTTGGTTATGACGGTTTGTATAT 540
DB |||||
577 AAGTGGACTTCAGATTACAGCAGTTTCCAAACCGCTTAGGTTATGACGGTTTGTATAT 636
QY |||||
541 TATTCCGGAGAACATCTCTTCCAAATCTTTACCGAGCGGGAACGCTGAAATATTCCCGC 600
DB |||||
637 TATTCCGGAGAACATCTCTTCCAAATCTTTACCGAGTGGGGAACGCTGAAATATTCTGCT 696
QY |||||
601 AACTGGCAATATATGACCGATGCGCATACGTCTCATCGAACAGAAAGCAGGAGATCTAGC 660
DB |||||
697 AACTGGCAATATATGACCGATGCGCATACGTCTCATCGAGCAGTAAAGC---GGTTGGCAT 753
QY |||||
661 GAAGATTTGGGTATATCGTTTATACGGTCAAAATGTGCGAGCAACTTCTTATGCTGCG 720
DB |||||
754 GACAATTTGGGTATATACATTTTATGGTAAACGATGTTGGTGCAACTTCTTATGCGGCT 813
QY |||||
721 ACTGCGAGCAGCGGAGGGAACATCTCGCAATATATCGTTTAAATTCGACCAAAAA 840
DB |||||
814 AAGGATGTGCGAGAAAGGGAACATCTCGTCAATATACGTTAGATTCGGTAAACAA 873
QY |||||
781 ACTCTGAATGCGCAAGCTGATTTAAATCAGTATGTGCAAAAGAGAGATGATCTTAAAAA 840
DB |||||
874 ACCCTGACGGCGAGCTGATTTAAACCAATATGTCMAACCCAGTGAGAAGC---AAAAA 930
QY |||||
841 CCACCTGACCATTTACGACATTTACTGCAAAATTTGGAGCGCAACCGCTTTACCGCGAGTGC 900
DB |||||
931 CGCTGACCATTTTCAACATCATCTCCGATTTTAAACGCGCAACCGCTTTACCGCGAGTGC 990
QY |||||
901 AAGTTAACAGAGGTGAGAGCATCAGCTGATATAAGATATTTGTTTTTCCATACC 960
DB |||||
991 AAGGTCAATCTCTGATTTAGCGAAAGCCATGCAATAGAGCATTTGTTTTCCATGCC 1050
QY |||||
961 GATGCGATCAGCGGCTTGAGGCGGTTTTTTCGGCGATAGGGGGAAGAGCTTGC CGGA 1020
DB |||||
1051 GATGCGGATCAGCGGCTTGAGGCGGTTTTTTCGGCGATAGGGGGAAGAGCTTGC CGGA 1110
QY |||||
1021 CGGTTTTATCAGCAACGACCAACAGCGTATTCGGGCTGTTGCGAGGCAACCAAAACAGAG 1080
DB |||||
1111 CGGTTTTATCAGCAACGACCAACAGCGTATTCGGGCTGTTGCGAGGCAACCAAAATAGCC-- 1168
QY |||||
1081 ACAGCAACGCAATCAGATCAAAATCTGCGCTCTCGGCTCTGGAACCAACACCAAAATCTTG 1140
DB |||||
1169 -----CGTGCCTCTGGAACCAACACCAAAATCTTG 1200
QY |||||
1141 GATTTCTAAATAATTTCCGTTGACGAGGCAAGTGGTGAATAATCCCGACCGTTGAGGTT 1200
DB |||||
1201 GATTTCTGAATAATTTCCGTTGATGAGGCAAGTGGTGAATAATCCCGACCGTTTGC CAT 1260
QY |||||
1201 TCCATATGCGCCGATTTGGTCAATCCGACAAACTTCTTTCGAGAGGCGCTGAAATTCCT 1260
DB |||||
1261 TCTCTATGCGCCGATTTGGTCAATCCGACAAACTTCTTTCGAGAGGCGATGAATTCCT 1320
QY |||||
1261 TTGGTAAACAAAGNACAAACCATGATCTTTCGCGAGCGGCAAGAAATGACCGCTCGTGCT 1320
DB |||||
1321 TTGGTTAGCAAGAGAAACCATTCAGCTTTCGCGAGCGGCAAGAAATGACCGCTCAGTGCT 1380
QY |||||
1321 TGTTCGCACTTTTTCAGCTATGTGAATCTCGAGCGGATTAATAACGGAAGCCCGCGCTC 1380
DB |||||
1381 TGTTCGCACTTTTTCAGCTATGTGAATCTCGAGCGGATTAATAACGGAAGCCCGCGCTC 1440

QY	1381	CAACGGAAGCGGCAGGATGAAGAGGGGGGACGAAGAGGGTCTAGCGTGTGATACGGTAAA	1440
Db	1441	AAACCGAAGGCGCA-----GGACGAAGAGGATTCGACACTTGATATGGCGAA	1488
QY	1441	GAAGCCGAAGACGAATCGCGCATGAAGAAGCACCGGAGACGAAGTCGTAGAAGATGA	1500
Db	1489	GAAGCGAAGACGAATCGCGCATGAAGAAGAGGACCGAAGATGCACCCGACGAGAT	1548
QY	1501	GACGAAGATGAAGACGAAGAGAAATCGAAGAGAACCTGAAGAAGAGCTGAAGAGGAA	1560
Db	1549	GAAGCCACGGAAGACGAAGCCACGAAGAACGAAGACGGCGAAGAACGACGAAGCTGAA	1608
QY	1561	GAACCCGAAGAAGAAATTCGCGCAGAGAAGAAAGGCAACGGCGTTTCAGGCAGCATCTGCCCC	1620
Db	1609	GAACCTGAAGAAGAAATCGTCGCG---AGAGGCAACGGCAGTTCAAACGCCATCTCGCCT	1665
QY	1621	ACTCCGGAGCGCTTAAGAGCAGGACATCGACCTTTTCTGAAAGGTATCCGCACGGCG	1680
Db	1666	GTCCCGAAGCGCTTAAGAGCGAGGATATCGACCTTTTCTGAAAGGTATCCGCACGGCA	1725
QY	1681	GAAGCCACACATTCCAAAGAACGGACCGCATATACGGGACATTGGGAAGCGGTATC	1740
Db	1726	GAACGATATTCGCGAACAATGGAGAGCACGCTATACCGGCACTTGGGAAGCGGTATC	1785
QY	1741	GGCGTATCGGATAGTGTAAGTCCATTCAAAGGATAGCTATGCG---AATCAGGGGCA	1797
Db	1786	GGC-----AAACCCATTCAATGGGACCATCATGCGGATTAAGAGCGGCA	1830
QY	1798	AAAGCAGAAATTAACGGTTGATTTGGAAGCGAAGACGGTGTCCGAATGCTGACAGAAAA	1857
Db	1831	AAAGCAGATATTACGGTTGATTTGGGCAAGAAATCGATTTCCGGAACGCTGACGAGAAA	1890
QY	1858	AATGATACACCCCGCTTTTATATTATTAAGAAAAAGGTGATGACGGTAACGGTTTCCAC	1917
Db	1891	AACGGTGTAGAACCTGCTTCCGTTATTAAGAACCGCGTGATTTGAGGCAACGGTTCCAT	1950
QY	1918	GCTTTGGCGGATACTCGGAGAACGGTATTGAACCTTCTCGGACAGGTTGACGCTAAACCG	1977
Db	1951	GGGACAGCGCGCACTCGGATGACGGCATCGACCTTTCGGGACAGGGTTGACCAAAACCG	2010
QY	1978	AAGAACTTCAGAGCCGACATCTTCTGTGAACAGCGCGCTTTTATGGCCCGCAGCGGCA	2037
Db	2011	CAGATCTTCAGAGCTAATGATCTTCTGTGTAAGAGGAGGATTTTACGGCCCGAAGGCGGAG	2070
QY	2038	GAATTGGCGGTAAATTTATCGACACCGACCGGAAATTCGGTCGGTATTTGGGGCGAAA	2097
Db	2071	GAATTGGCGGTATTTATTTTCAATATGATGGGAATCTCTTGGTATAACTGAAGGTACT	2130
QY	2098	AAAGATGACAGGAGGC	2114
Db	2131	GAATAAAGTTGAAGC	2147

RESULT 8
AAX23322

ID AAX23322 standard; cDNA; 2262 BP.

AX
AC

XX
DT 11-JUN-1999 (first entry)

XX
DE
vv

LbpB; lactoferrin binding protein; vaccine; neisserial disease; meningitis; diagnosis; treatment; ds.

OS *Neisseria meningitidis*.

XX	
PH	Key
FT	CDS
FT	1. .2262
FT	/*tag= a
FT	/product= "LbpB"
XX	

W03909176-A1.
25-FEB-1999.
10-AUG-1998; 98WO-EP005117.
15-AUG-1997; 97GB-00017423.
05-FEB-1998; 98GB-00002544.
(UYUT-) RIJKSUNIV UTRECHT.
(TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
Petterson-Fernholm AM, Tommassen JPM;
WPI; 1999-190165/16.
P-PSDB; AAW93495.
New lactoferrin-binding protein B polynucleotides - obtained from
Neisseria meningitidis, used to develop products for the diagnosis,
prevention and treatment of neisserial disease, e.g. meningitis.
Claim 2; Page 98-102; 116pp; English.
This invention describes novel lactoferrin-binding protein B (LbpB)
strains of Neisseria meningitidis. The products of this invention can be
used for vaccinating humans against neisserial disease e.g. meningitis.
CC Antibodies raised against the proteins of the invention can be used for
CC diagnosing or treating neisserial disease in humans. The LbpB
CC polypeptides can also be used for identifying compounds which inhibit the
CC polypeptides
Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;
Query Match 60.8%; Score 1291.8; DB 2; Length 2262;
Best Local Similarity 78.1%; Pred. No. 7.1e-311;
Matches 1676; Conservative 0; Mismatches 417; Indels 54; Gaps

QY	1	ATGTGTAACCGAATTATGGCGGCAATGCTCTGTGTGGCCCTTACTTTTGGCATCTTGGCATC	50
Db	1	ATGTGTAACCGAATTATGGCGGCAATGCTCTGTGTGGCCCTTACTTTTGGCATCTTGGCATC	60
QY	61	GGCGGCAATTTGGCGGTGCAGCTTGTGTGCAATCAAGCGCGAAGCGCGG-----	108
Db	61	GGCGGCAATTTGGCGGTGCAGCTTGTGTGCAATCAAGCGCGAAGCGCGG-----	108
QY	109	TACCCCGTCACTTTTCAAGTCTAAGGACGTTCCCACTTTCGCCCTCTCGCGGTCTTCGGTA	168
Db	121	GATTCCAAAATCTTCCCAATCTTCGCGATAAGCCTGCTCAGTCTCTGCGAGCCTTCGGTA	180
QY	169	GAACACGACGGGTCAACGACCGCGCGTGTGGTCGGCAATGCGGCTGTGTGAGACGGAAT	228
Db	181	GAATACGCGCGGTCAAGCGCGCGCGCGTGGTGGGCAATGCGGCTGCCAAGCGGAAT	240
QY	229	ATTGCAACTTCTGATAAGGATGCAATGATTTTCCAAATAGCAAAAAGCGGCTGAGACGGAAT	288
Db	241	ATCGCACTTTGATTAATAAGTATGTAATAATGCCAATAGTAAGCAGGCGAGGAGTAT	300
QY	289	CTGTGCTTTAAGAGGAAGATATCCTGTTTTTATACGTTTCCAAAAGAGATCAACGTCAG	348
Db	301	CTCGCGCTCAAGAGAAGGATATCCTGTTTTTATAGACGTTACGCCGAAGAACAGGCTGAC	360
QY	349	CAGCTTTAAGATAAAATTCGTCAACCAATCTTACGGCAAGCATTCACCATCGGAAAAG	408
Db	361	AAACTTTAAAAGGAAATCAACGAGCGGATCTTAATGACCAATCTACAGTCCGATTTA	420
QY	409	AAAAATAAAAAATATGATTATATAATTTGTAGATGCAAGTTATGTATATATACTAAGACGGA	468
Db	421	AAAGATGATCGGTATCAATATATAATATGTCGCGGCGGATATGTTTTATCTAGATATGGA	480
QY	469	AAAGATGAAATGAGTGGACTTCAAATTAACAAGCAGTCTTACCACCGGTTTGGTTATGAC	528
Db	481	ACAGATGAAATCGAACAGAACTCAGGCGGTAAAGCGGTTACCCACGCTTAGGTTATGAC	540

QY	529	GGTTTGTATATATTCGGAGAACATCTCTTCCGATCTTTTACCGAGCGGGAACGGTG	588	DB	1615	GGCAACGGCGGTTTCAGGCGCATCTCTGCTTGCCTTAGAACCTCTTAAGCAGGCGCATC	1674
DB	541	GGTTTGTATATATTCGGAGAACATCTCTTCCGATCTTTTACCGAGCGGGAACGGTG	600	QY	1651	GACCTTTCTCTGAAGGTATCCGACGGCGGAAGCCGACATTCCTCAAAAAACGGAACGGCG	1710
QY	589	AAATATTCGGGAACTGGGCAATATATGACCGATGCGCATAGTGTATCGAAGCAAGCA	648	DB	1675	GACCTTTCTCTGAAGGTATCCGACGGCGGAAGCCGATATTCGCAAAACGGGAACGGCG	1734
DB	601	GAATATTCGGTAACTGGGCAATATATGACCGATGCGCAAGCTGTATCGAAGGTTCAGC	659	QY	1711	CATTATACCGGCACTTTGGGAAGCGGTATCGGCGTATCGGATAGTGTATCGTCCATTCAA	1770
QY	649	GGAGATCTAGCGAAGATTTGGGTATATATCGTTTATACGGTCAAAATGTCGAGCAACT	708	DB	1735	CATTATACCGGCACTTTGGGAAGCGGTATCGGCGTATCGGCGTATCGGCGTATCGGCG	1779
DB	660	--GGTGGCATTTGACATTTGGGTATATATCACAATTTTATGTAACGATGTTGGTCAACT	717	QY	1771	AAGATAGCTATCGGAT---CAAGGGCAAAAGCAGAAATTTACGTTGATTTTCAAGCG	1827
QY	709	TCTTATCTCGCATCTGCGACGACCGGGAGGGAAGAAATCTCTGCGGATATACGGTTAAT	768	DB	1780	TGGGACAAATCAGCGCGGATGAAAAGCGGCAAAAGCAGAAATTTACGTTGATTTTCAAG	1839
DB	718	TCTTATCGGCTAAGATGTCCAGAAAGGGAAGCATCTCTGCAAAATATACGGTTGAT	777	QY	1828	AAGACGGTGTCCGGAATGCTGACAGAAAAAAATGATACAAACCCCGCTTTTATATTGAA	1887
QY	769	TTGACCAAAAACCTCTGAATGCGCAAGCTGATTAATAATCATGATGTGC---AAAAAGA	825	DB	1840	AAATCGAATTTCCGGAAGCTGACGGAGCAAAACCGGTAGAACCTGCTTTCATATTGAA	1899
DB	778	TTTGATAACAAACCATGAATGGCAAGCTGATTAATAATCATGATGTGC---AAAAAGA	837	QY	1888	AAAGGTGTGATGACGGTAAACGGTTTCAACGCTTTGGCGCATACTCGGAGAACGGTATT	1947
QY	826	GATGATCTTAAAAACCACTGACCATTTTACGACATTTACTGCAAAATTTGACGCGCAACCG	885	DB	1900	GACGGCAAGATTTGATGCAACGGTTTCCACGCGACAGCGCGCATCTCGGAGAGCGGCATC	1959
DB	838	GATGACCAAAACCGCTGACCATTTTACGACATTTACTGCAAAATTTGACGCGCAACCG	897	QY	1948	GACCTTTCTGGCAGGGTTTCGACTAACCCGGAAGAACTTTCAAGCGCAACATCTTCTTCTTA	2007
QY	886	TTTACCGGCACTGCAAAAGTTAAACAGAGGTGAAGACGATCACGCTGATAAAGATAT	945	DB	1960	AATCTTTCCGGAATTTGTTGACCGACCCCAAAATTTCCAAAGCTAGTAATCTTCTGCTTA	2019
DB	898	TTTACCGGCACTGCAAAAGTTAAACAGAGGTGAAGACGATCACGCTGATAAAGATAT	957	QY	2008	ACAGCGCGCTTTTATGCGCCCGCAGCGCAGAAATTTGGCGGTAATATTATCGACAGCGAC	2067
QY	946	TTGTTTTTCCATACCGATGCGCATCAGCGGCTTGAGGCGGTTTTTTCGGCGATTAAGGG	1005	DB	2020	GAAGAGATTTTACGCGCCCGCAGCGCGGGAATTTGGCGGTAATATTATCGACAGCGAC	2079
DB	958	TTGTTTTTCCATACCGATGCGCATCAGCGGCTTGAGGCGGTTTTTTCGGCGATTAAGGG	1017	QY	2068	CGGAAATCTCTTAGTATACTGAAATATTTGAAAATGAACTGAAAGC	2114
QY	1006	GAAAGAGCTTGCAGGCGGTTTTATCAGCAACGACAGCGTATTCGGCGTGTTCGAGCG	1065	DB	2080	GGGAAATCTCTTAGTATACTGAAATATTTGAAAATGAACTGAAAGC	2126
DB	1018	GAAAGAGCTTGCAGGCGGTTTTATCAGCAACGACAGCGTATTCGGCGTATTCGAGCG	1077	RESULT 9			
QY	1066	AAACAAAAACAGAGACGAAACGATCAGATACGATACGATACGATACGATACGATACG	1125	AAA81482/c			
DB	1078	A---AAAAACAGAGACGAAACGAGAGATACGATACGATACGATACGATACGATACG	1134	ID	AAA81482	standard; DNA; 14652 BP.	
QY	1126	CACACCAAAATCTTGATTTCTTAAATAATTTCCGTTGACGAGGCAAGTGTGAAATCCC	1185	XX	AAA81482;		
DB	1135	CACACCAAAATCTTGATTTCTTAAATAATTTCCGTTGACGAGGCAAGTGTGAAATCCC	1194	XX	04-DEC-2000	(first entry)	
QY	1186	CGACCGTTTTCAGTTTCCATATGCGCGATTTTGGTATCCCGCAAACTTCTTTCGAA	1245	DE	N. meningitidis	partial DNA sequence gnm_30	SEQ ID NO:30.
DB	1195	CGTAAAGTTGCGATTTCTCTATGCGCGATTTTGGTATCCCGCAAACTTCTTTCGAA	1254	XX	Neisseria meningitidis;	Neisseria gonorrhoeae; genome; immunogenic;	
QY	1246	GGCGGTGAATTCCTTTGGTAAACAGAACCAACCATGATCTTCCGACGCGCAGAA	1305	KW	antigen; vaccine; diagnosis; infection; antibacterial; identification;		
DB	1255	GGCGGTGAATTCCTTTGGTAAACAGAACCAACCATGATCTTCCGACGCGCAGAA	1314	KW	Meningococcus B; MenB; ds.		
QY	1306	ATGACGCTCGCTGCTTGTTCGCGATTTTTCGACCTATGTAACCTCGGACGATTAATAAC	1365	XX	Neisseria meningitidis.		
DB	1315	ATGACGCTCGCTGCTTGTTCGCGATTTTTCGACCTATGTAACCTCGGACGATTAATAAC	1374	PN	W0200022430-A2.		
QY	1366	GAAACGCCCCCGCTCCAAACGAGCGGCAAGATGAAGAGGGGAGAGAGGGGTGAGGC	1425	XX	20-APR-2000.		
DB	1375	GATCGCCCGCAAGTAAACCAAGCGGCAAGATTAAGGGGAGGATGAAGAGGGGTGAGGC	1434	XX	08-OCT-1999;	99WO-US023573.	
QY	1426	GTTGATTAACGGTAAAGAGCGAGAGCAATCGCGATGAAGAAAGCACCGGAGACGAA	1485	XX	09-OCT-1998;	98US-0103794P.	
DB	1435	GTTGATTAACGGTAAAGAGCGAGAGCAATCGCGATGAAGAAAGCACCGGAGAGAC	1494	XX	30-APR-1999;	99US-0132068P.	
QY	1486	G-----TCGTAGAGATGAAGACCAAGATGAAGA-----CGAAGAAAGAAATCGAA	1530	XX	(CHIR)	CHIRON CORP.	
DB	1495	GAACTTCCGAGAGGATTAATGGCGAAGACGAGAGCAACCGCGAAGAAAGCAACCGAA	1554	XX	Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;		
QY	1531	GAAAGACCTGAAGAAAGAGCTGAAGAGAGAAACCCGAGAGAAATTCGCGGACAGAA	1590	PI	Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;		
DB	1555	GAAAGTTGATGAAGCCGAGAGAGAGGAGGATTTGAAGAACCCGAGAGAAATTCGCGGAC	1614	PI	Rappuoli R, Pizza M;		
QY	1591	GGCAACGGCGGTTTCAGGAGCATCTGCGCCATCTCGGCAAGCTCTTAAAGGCGGAGCATC	1650	XX	WPI; 2000-318079/27.		

Isolated nucleotide sequences of *Neisseria meningitidis* which can be used in the diagnosis and treatment of *N. meningitidis* infection and other *Neisseria* infections, for example, *N. gonorrhoea*.

Claim 7; Page 582-586; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent specifically claimed *Neisseria meningitidis* genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of *Neisseria meningitidis* DNA sequences; and AAA81452 represent *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to *Neisseria* bacteria. For example, some of the identified proteins could be components of vaccines against *Meningococcus B*; against all serotypes; and/or against all pathogenic *Neisseria*. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious *Meningococcus B* vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions

Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;

PS	Query Match	44.1%;	Score 937.4;	DB 3;	Length 14652;
XX	Best Local Similarity	81.2%;	Pred. No. 2.3e-22;		
	Matches 1155;	Conservative	0;	Mismatches 226;	Indels 42; Gaps 4;
QY	703	GCAATCTTATGTCGGACTCGCGACGACCGGAGGGAACATCTCTCCGAATATACG	762		
Db	14652	GCAATCTTATGTCGGACTCGCGACGACCGGAGGGAACATCTCTCCGAATATACG	14593		
QY	763	GTTAAATTCGACCAAAACCTCAATGGCGAGCTGATTAATAATCAGTATGTCGAAAG	822		
Db	14592	GTTGATTTTGATACAAACCCCTGAATGGCAAGCTGATTAATAATCAGTATGTCGAAAT	14533		
QY	823	A-----GAGATGATCTCTAAAAACCACTGACCATTTTACGACATTACTTGCAAAATTG	873		
Db	14532	AAAAGTAATCAATGAGCCCAAAAACCGCTGACATTTACGACATTTACCGCAACATTG	14473		
QY	874	GAGCGCAACCGCTTACCGGAGTGCCAAAGTTAAACACAGAGTGGAAGCAATCAAGCT	933		
Db	14472	GACGGCAACCGCTTACCGGAGTGCCAAAGTTAGCACCGAGGTGAAGACGCAACGCT	14413		
QY	934	GATAAAGAAATATTGTTTTCATACCGATCCGATCCGATCCGATCCGATCCGATCCG	993		
Db	14412	GATAAAGAAATATTGTTTTCATACCGATCCGATCCGATCCGATCCGATCCGATCCG	14353		
QY	994	GCGGATAAGGGGAAGAGCTTGCAGGACGGTTCATCAGCAACGACACGACGATTCGGC	1053		
Db	14352	GCGGATAACGAGAGAGCTTGCAGGACGGTTCATCAGCAACGACACGATTCGGC	14293		
QY	1054	GTCTTCGAGGCAACAAACAAACAGACAGCAAAACGATCAGATCAAACTCTGCCCTG	1113		
Db	14292	GTATTCGAGGCAACAAACAAACAGACAGCAAAACGATCAGATCAAACTCTGCCCTG	14233		
QY	1114	CCGTCTGGAACACACACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGGCAAGT	1173		
Db	14232	TCGTCTGGAACACACACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGGCAAGT	14173		
QY	1174	GGTGAATAATCCCGACCGCTTTCAGGTTTCCACATATCCCGATTTTCGTATCCCGACAA	1233		
Db	14172	GATAAATAATCCCGACCGCTTTCAGGTTTTCGTATCCCGATTTTCGTATCCCGACAA	14113		
QY	1234	CTTCTTGTGAGGGGCTGAATTCCTTGGTAAACAAAGCAACACCATCGATCTTGGC	1293		
Db	14112	CTTCTTGTGAGGGGCTGAATTCCTTGGTAAACAAAGCAACACCATCGATCTTGGC	14053		

QY	1294	GACGGCAGCAAAATACCGCTCGTGCTTCTGCGACTTTTGTGACCTATGTGAAACTCGGA	1353		
Db	14052	GATGTTAGGAAACGACAACTCGAACCTCTGCTGATTTTCTGTGACCTATGTGAAACTCGGA	13993		
QY	1354	CGGATAAAACCGAAGCGCCCGCCGCTCCAAACCGAAGCGCGCAGGATCAAGAGGGGGACGAA	1413		
Db	13992	CGGATGCAAAACCGAAGCGCTCCCGCCGCAACCGAAGCGCGCAGGACGAAGAGGGGACGAA	13933		
QY	1414	GAGGGTGTAGGGGTTGATAACCGTTAAAGAACGAGAGCAATTCGGCGATCAAGAAAGC	1473		
Db	13932	GAGGATACAGGGGTTGATAGCTCGAAGAGGCGAAGCAATTCGACGATCAAGAGGC	13873		
QY	1474	ACCGGAGACGAAGTCTGTAAGATCAAGACGAAGATGAAGACGAAGCAAGCAATTCGAGAA	1533		
Db	13872	ACCGAAGACGACCGCTAAAGACGAAGCGCAGGAGGAAGAGCAAGACCGTA-----	13822		
QY	1534	GACCTGAAGAAAGCTGAAGAGGAAGAACCCGGAAGAAATTCGCGCGCAGAAAGGC	1593		
Db	13821	-----GAAGGTGAAGATGAAGCTGAAGAACCCGGAAGAAATTCGCGCGCAGAAAGGC	13768		
QY	1594	AACGCGGCTTCAGGCAGCATCTGCCCCACTCGGAAGCCTCTAAAGGAGGAGCATCGAC	1653		
Db	13767	GGCAGCGGTTGAGACGCGCATCTGCCCCCTCGGAAGCCCTAAAGGAGGAGCATCGAC	13708		
QY	1654	CTTTTCCTGAAAGGTATCCGCAACCGCGGAGCGACATTTCCCAAAACCGAACCGCGCAT	1713		
Db	13707	CTTTTCCTGAAAGGTATCCGCAACCGCGGAAACGGATATTCGGAACCTGGAGAAAGCAC	13648		
QY	1714	TATACCGGCACTTCGGAAGCGCTATCGGCGTATCGGATGTGCTGCTCATTTCAAAAG	1773		
Db	13647	TATACCGGCACTTCGGAAGCGCGTATCGGC-----AAACCCATTTCAATGG	13603		
QY	1774	GATAGCTATGCG---AATCAAGGGGAAAAGCAGAAATTTACGTGATTTCCGAAGCGAAG	1830		
Db	13602	GACAAATCAGGCGGATTAAGAAAGCGGCAAAAGCAGTATTTACCGTTGATTTTCGCAAGAA	13543		
QY	1831	ACGCTGTCCGGAATGCTGACAGAAAAAATGATACACCCCGCTTTTATATTTGAAAAA	1890		
Db	13542	TCGATTTCCGGAAGCTGACGAGGAAACCGGTGAGAACCTGCTTTCCATTTATTTGAAAC	13483		
QY	1891	GGTGTGATGACGGTAAACGGTTTCCAGCTTTCCGCGCATCTCGGAGAGACGGTATTGAC	1950		
Db	13482	GGCAAGATTGAGGCAACGGTTTCTACCGCACACGACGCTCGGAGAGACGGCATCAAT	13423		
QY	1951	CTTTCGGGAGGTTGCACTAACCCGAGAACTTCAAGCCGCAAACTCTTTCTTTGTAACA	2010		
Db	13422	CTTTCCGGAATGGTTCCGACCGACCCCAAAACCTTCCAGCTAGTATCTTCGTGTAGAA	13363		
QY	2011	GGCGGCTTTTATGGCCCGCAGCGCGCAGAAATTCGGCGGTAAATTCGACAGCGACCG	2070		
Db	13362	GGGGGATTTTACGCGCGCAGCGGAGGAATTCGGCGGTATTTTTCATTAATGATGGG	13303		
QY	2071	AAATTCGTCGGTATTTGCGGCGAAAAAAGATGACAAAGGAGG	2113		
Db	13302	AAATCTCTGGTATACTGAAGGTACTGAAAAATAAGTTGATG	13260		

RESULT 10

AAF91389

ID AAF91389 standard; DNA; 1000 BP.

XX AAF91389;

XX AAF91389;

DT 04-MAY-2001 (first entry)

XX N. meningitidis

(serogroup B) LbpA gene upstream sequence, SEQ ID:15.

DE Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine;

XX genetically modified; protective antigen expression; LPS detoxification;

KW LPS; lipid A; homologous recombination vector; immunisation;

KW immunoprotective; non-toxic; paediatric; cyclic; circular; ds.

XX

Thu Aug 26 10:18:19 2004

OS	Neisseria meningitidis.	
XX	WC200109350-A2.	
PN		
XX		
PD	08-FEB-2001.	
XX		
PF	31-JUL-2000; 2000WO-EP007424.	
XX		
PR	03-AUG-1999; 99GB-00018319.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.	
XX		
PI	Berthet FJ, Dalemans WLJ, Denoel P, Dequesne G, Feron C, Lobet Y;	
PI	Poolman J, Thiry G, Thonnard J, Voet P;	
XX		
DR	WPI; 2001-138654/14.	
XX		
PT	New isolated polynucleotide useful for outer membrane vesicle preparation	
PT	from Gram-negative bacterial strain for vaccination of microbial	
PT	infections.	
XX		
PS	Claim 46; Page 81; 128pp; English.	
XX		
CC	The invention relates to a genetically-engineered outer membrane vesicle	
CC	(bleb) preparation from a Gram-negative bacterium for use as a vaccine.	
CC	The blebs of the invention are improved with respect to their	
CC	immunogenicity and toxicity by the introduction of one or more genetic	
CC	changes to the chromosome of the bacterium from which the blebs are	
CC	derived. The changes made include the upregulation of protective antigen	
CC	expression, the downregulation of immunodominant non-protective antigen	
CC	expression, and genetic changes which result in detoxification of the	
CC	Lipid A moiety of lipopolysaccharide (LPS). The invention also	
CC	encompasses modified Gram-negative bacterial strains from which the bleb	
CC	preparations are made, a vector suitable for performing recombination	
CC	events (for the generation of the modified bacterial strains),	
CC	bacterially-derived nucleic acid sequences used in such a vector, and an	
CC	immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole	
CC	cell vaccine suitable for paediatric use. The bleb preparation is useful	
CC	in the manufacture of a medicament for immunising a human host against a	
CC	disease caused by infection of one or more of the following: Neisseria	
CC	meningitidis, Neisseria gonorrhoeae, Haemophilus influenzae, Moraxella	
CC	cattarrhalis, Pseudomonas aeruginosa, Chlamydia trachomatis, and Chlamydia	
CC	pneumonia. The invention may also be used to provide immunisation against	
CC	the influenza virus. Bacterially derived nucleotide sequences of the	
CC	invention are used in the performance of homologous recombination events	
CC	up to 1000 bp upstream of a bacterial chromosomal gene in order to either	
CC	increase or decrease expression of that gene. Immunoprotective and non-	
CC	toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more	
CC	immunogenic, less toxic and safer, and are particularly useful for	
CC	paediatric use. The present sequence represents a specifically claimed	
CC	Neisseria meningitidis nucleic acid sequence	
XX		
SQ	Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;	
	Query Match 23.4%; Score 497.6; DB 4; Length 1000;	
	Best Local Similarity 75.8%; Pred. No. 2e-113;	
	Matches 679; Conservative 0; Mismatches 189; Indels 28; Gaps 4;	
QY	1213 GATTTTGGTCTATCCCGACAACTCTTGTGCGAGGGCGTGAATTCCTTTGGTAAACAA 1272	
DB	1 GATTTTGGTCTATCCCGACAACTCTTGTGCGAGGGCGTGAATTCCTTTGGTAAACAA 60	
QY	1273 GAACAAACCATCGATCTTCGCGAGCGCAGGAAATGACCGTCCGTCCTTTGTCGACTTT 1332	
DB	61 GAGAAACCATCAAGCTTCGCGATGCGAGGAAATGACCGTCCGTCCTTTGTCGACTTT 120	
QY	1333 TTGACCTATGTGAATTCGACCGATAAACACCGCCCGTCCAAACCGAAGGCG 1392	
DB	121 TTGACCTATGTGAATTCGACCGATAAACACCGCCCGTCCAAACCGAAGGCG 180	
QY	1393 CAGGATCAAGAGGGGACGAGAGGGGTGTAGCGCTTGATTAACGGTAAAGAACGCGAGAC 1452	
DB	181 GAAGATAAAGGGAGGATGAAGAGGTGCAGCGGTGGTAAACGTCGAAGAAGCGAAGGC 240	

QY	1453 GAAATCGCGATGAAGAAGACACCGAGAGCGAAGTCTGTAGAGATGAAGACGAGATGAA 1512	
DB	241 GAAATTCGCGAAGTGA-----AGCGAAGAAGCCGAGAAATCGTCTGAAGAAGAA 291	
QY	1513 GACGAAGAAGAAATCGAAGAAGAACCTGGAAGAAGAGCTGAAGAGGAGAACCCGAGAA 1572	
DB	292 CCCGAAGAAGAGCTGAAGAGAGGAAGCTGAAACCCCAAGAGAGTTGAAGAAACCGAAGAA 351	
QY	1573 GAAATTCGCGCAGAAGAAGCGGCGTTTCAGGAGAGCATCTTCGCCACTTCGCGAAGCC 1632	
DB	352 AAATTCGCGCAGACGAAGAAGCGGCGGTTTCAACGCCATCTCTGCTCTCTCGAAGACC 411	
QY	1633 TCTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGACGCGGCGAAGCCGACATT 1692	
DB	412 TCTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGACGCGGCGAAGCCGACATT 471	
QY	1693 CCAAAAAACGGAACGCGCGCATTTATACCGGCACCTTGGGAAGCGGTATCGGATTCGAT 1752	
DB	472 CCAAGAACCGGAAGAACGACATATACCGGCACCTTTGGGAAGCGGTATCGGC----- 522	
QY	1753 AGTGGTACGTCATTCAAAAAGGATAGCTATGCG---AATCAAGGGGCAAAAAGCAGAAATTT 1809	
DB	523 -----ACACCCATTCAATCGGACATACGCGCGATTAAGAGCGGCAAAAGCAGAAATTT 576	
QY	1810 ACCGTTGATTTTCGAAGCGAAGACGCGTCTCGGAATGTGACAGAAAAAATGATACAAACC 1869	
DB	577 ACCGTTAATTTTCGCGAGAAATCGATTTTCGGAACGCTGACGAGAGAAAAACGGTGTACAA 636	
QY	1870 CCOCCTTTTATATGAAAAAGGTGTGATTCACGTTACGTTTCCAGCGTTTGGCGCAT 1929	
DB	637 CCGTCTTTTATATGAAAAACGCGCAAGATTGAGGCGCAACGGTTTCCAGCAACAGCACGC 696	
QY	1930 ACTCGGAGAGCGGTATTGACCTTTTCGCGCAGGCTTCGACTAACCCGAAAGAACTTCAAA 1989	
DB	697 ACTCGTGAAGACGCGCATCAATCTTTCGGAATGTTGTCGACCAACCCAGAACCTTCCAA 756	
QY	1990 GCCGACAACTTTCTTTGTAAACAGCGCGCTTTTATGCGCGCAGCGCGGCGAATTTGGCGGT 2049	
DB	757 GCTAGTGATCTTCGTGTAGAGGAGGATTTTACGCGCGCGCA--GCGAGGAAATTTGGCGGT 815	
QY	2050 AATATTATCGACAGCGACCGGAAATTCGTCGGTGTATTTCGGGCGCAAAAAGATCA 2105	
DB	816 ATTATTTTCAATAGGATGGGAAATCTCTGTATATACTGAAGGTACTGAAATAA 871	
	RESULT 11	
	ABK37769	
ID	ABK37769 standard; DNA; 1000 BP.	
AC	ABK37769;	
XX		
DT	08-MAY-2002 (first entry)	
DE	DNA sequence upstream of LbpA #1 gene.	
XX		
KW	Upstream sequence; ds; Antibacterial; vaccine; bleb;	
KW	Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;	
KW	meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;	
XX	sinusitis.	
OS	Neisseria meningitidis serogroup B.	
XX		
PN	WO200209746-A2.	
XX		
PD	07-FEB-2002.	
XX		
PF	31-JUL-2001; 2001WO-EP008857.	
XX		
PR	31-JUL-2000; 2000WO-EP007424.	
PR	08-FEB-2001; 2001GB-00003170.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.	

XX Berthet FJ, Dalemans W, Denoel P, Dequesne G, Feron C, Garcon N;
 PI Lobet Y, Poolman J, Thiry G, Thonnard J, Voet P;
 XX WPI; 2002-188698/24.
 XX
 PT New immunogenic composition comprising an antigen derived from a pathogen
 PT and a blep preparation from *Neisseria meningitidis*, useful as a vaccine
 PT for treating or preventing disease caused by the pathogen.
 XX
 PS Disclosure; Page 84; 125pp; English.
 PS
 CC The invention relates to an immunogenic composition comprising an antigen
 CC derived from a pathogen capable of protecting a host against the
 CC pathogen, mixed with an adjuvant comprising a blep preparation derived
 CC from a Gram-negative bacterial strain. The immunogenic composition
 CC consists of *N. meningitidis* B blebs or *N. meningitidis* C polysaccharide
 CC antigen. The blebs (derived from the outer membrane) may also have their
 CC toxic lipopolysaccharide (LPS) content reduced using heterologous down
 CC regulating sequences for LPS pathway genes or by up regulating genes
 CC involved in LPS synthesis suppression, by a promoter replacement
 CC technique. The immunogenic preparation is useful in the manufacture of a
 CC medicament for the treatment of a disease caused by the pathogen from
 CC which the antigen is derived (e.g. from *Neisseria meningitidis* and
 CC bacteraemia, from *Moraxella*, otitis media and pneumonia, and from *H.*
 CC *influenzae* chronic bronchitis, sinusitis, pneumonia and otitis media).
 CC The bleb derived from *M. catarrhalis* or from a non-typeable *H. influenzae*
 CC is useful as an adjuvant in an immunogenic composition comprising one or
 CC more pneumococcal capsular polysaccharides or protein antigens. The
 CC present sequence is an upstream sequence from an *N. meningitidis*,
 CC *H. influenzae* or *M. catarrhalis* gene involved in LPS biosynthesis, which
 CC either up regulates or down regulates sequences to which it is attached
 CC
 XX SQ Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;
 XX
 Query Match 23.4%; Score 497.6; DB 6; Length 1000;
 Best Local Similarity 75.8%; Pred. No. 2e-113;
 Matches 679; Conservative 0; Mismatches 189; Indels 28; Gaps 4;
 QY 1213 GATTTCGTCTATCCGACAACTCTTCTGCAAGGGCGTGAATTCCTTGGTAAACAAA 1272
 DB 1 GATTTCGTCTATCCGACAACTCTTCTGCAAGGGCGTGAATTCCTTGGTAAACAAA 60
 QY 1273 GAACAAACCATCGATCTTCCGACGCGAGGAAATGACCGTCCGTCTGTTGCGACTTT 1332
 DB 61 GAGAAAACCATCAAGTTGCGATGCGGAGGAAATGACCGTCCGTCTGTTGCGACTTT 120
 QY 1333 TTGACCTATGTGAACCTCGACGGATAAACCGAACGCCCGCTCCAAACCGAAGCG 1392
 DB 121 TTGACCTATGTGAACCTCGACGGATAAACCGAACGCCCGCTCCAAACCGAAGCG 180
 QY 1393 CAGGATGAAGAGGGGACGAAGAGGTGTAGCGTTGATTAACCGTAAAGAACGGAAGAC 1452
 DB 181 GAAGATAAAGAGGAGGATGAAGAGAGTGCAGGCGTTGGTAAACGTCGAAGAGCGAAGC 240
 QY 1453 GAAATCGGCGATGAAGAAACACCGGAGACGAAGTCTGTAAGATGAAGACGAAGATGA 1512
 DB 241 GAAGTTCCGACATGA-----AGGCAAGAGACCGGAAGAAATCGTCGAAGAGAA 291
 QY 1513 GACGAGAGAAATCAAGAGAACCTGAAGAGAGAGCTGAAGAGGAAGAACCCGGAAGAA 1572
 DB 292 CCGAAGAGAGAGCTGAAGAGGAAGAGAGCTGAACCCAAAGAGTGAAGAAACCGAAGAA 351
 QY 1573 GAATTCGCCGACAGAAAGCAACGCGGTTCAGGAGCATCTCGCCCATCTCGGAAGCC 1632
 DB 352 AATTCGCCGACAGAAAGCAACGCGGTTCAGGAGCATCTCGCCCATCTCGGAAGCC 411
 QY 1633 TCTAAGGAGGAGACATCGACCTTTTCTGAAAGGTATCCGACGCGGAAGCCGACATT 1692
 DB 412 TCTAAGGAGGAGACATCGACCTTTTCTGAAAGGTATCCGACGCGGAAGCCGACATT 471
 QY 1693 CCAAAACCGAAGCGGCGCATATACCGCATCTTGGGAAGCGCGTATCGGCGTATCGGAT 1752

Db 472 CCAAGAACCGGAAAAAGCACATATACCGGCACCTTGGGAGCGCGTATCGGC----- 522
 QY 1753 AGTGGTAGCTCCATTCAAAAGAGTAGTATGCG---AATCAAGGGGCAAAAGCAGAAATTT 1809
 Db 523 -----ACACCCATTCAATGGGCAATCAGCGCGGATAAAGAGCGGCAAAAGCAGAAATTT 576
 QY 1810 ACGTTGATTTGGAACGAGACGGTGTCCGGAATCTGACAGAAAAAATGATACAAACC 1869
 Db 577 ACGTTAAATTCGGCGAGAAATCGATTCGGAACGCTCAGGAGAAAAACGGTGACAA 636
 QY 1870 CCGCTTTTATATTGAAAAAGGTGATGACGGTAAACGGTTTCCACGCTTTGGCGCAT 1929
 Db 637 CTGCTTTTATATTGAAAAACGCAAGATTGAGGCAACGGTTTCCACCAACAGACGC 696
 QY 1930 ACTCGGAGAACGGTATTGACCTTTCTGGCAGGGTTCGACTAACCCGAAGAACTTCAA 1989
 Db 697 ACTGTGAGACGGCATCAATCTTTGGGAAATGGTTGACCAACCCAGAACCTTCCAA 756
 QY 1990 GCCACAATCTTCTTTGTAACAGCGCGCTTTTATGCGCGCAGCGCAGAAATTTGGCGGT 2049
 Db 757 GCTAGTGAATCTTCGNGTAGAGGAGATTTTACGGCCCGCA-GCGAGGAATTTGGCGGT 815
 QY 2050 AATATTATCGACAGCGACCGGAAATTCGGTTCGGTATTGGCGCGAAAAAGATGA 2105
 Db 816 ATTATTTTCAATAGGATGGGAAATCTCTTGGTATACTGAAGGTACTCAAAATAA 871
 XX
 RESULT 12
 AAA81815
 ID AAA81815 standard; DNA; 707 BP.
 XX
 AC AAA81815;
 XX
 DT 04-DEC-2000 (first entry)
 DE N. meningitidis partial DNA sequence gnm_362 SEQ ID NO:362.
 XX
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW *Meningococcus B*; MenB; ds.
 XX
 OS *Neisseria meningitidis*.
 XX
 FN WO200022430-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US023573.
 XX
 PR 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 PI Rappuoli R, Pizza M;
 XX
 DR WPI; 2000-318079/27.
 XX
 PT Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
 PT in the diagnosis and treatment of *N. meningitidis* infection and other
 PT *Neisseria* infections, for example, *N. gonorrhoea*.
 XX
 PS Claim 7; Page 1606; 1760pp; English.
 XX
 CC The present invention describes methods of obtaining immunogenic proteins
 CC from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent

CC Neisseria meningitidis MenB polynucleotide ORF sequences, which are all
CC used in the exemplification of the present invention. The nucleic acid
CC sequences, protein sequences, and antibodies against them, can be used in
CC the manufacture of a composition. The composition can be used as a
CC medicament (or in the manufacture of a medicament) for treating,
CC preventing or diagnosing infection due to Neisserial bacteria. For
CC example, some of the identified proteins could be components of vaccines
CC against Meningococcus B; against all serotypes; and/or against all
CC pathogenic Neisseriae. Identification of sequences from the bacterium
CC will also facilitate production of biological probes, particularly
CC organism-specific probes. Attempts to make efficacious Meningococcus B
CC vaccines have failed mainly due to antigen tolerance. Multivalent
CC vaccines have also been tried but none have successfully overcome
CC antigenic variability. The provision of further, complete sequences may
CC provide an opportunity to identify secreted or surface exposed proteins
CC that may be presumed targets for the immune system and which are not
CC antigenically variable or at least more conserved than other more
CC variable regions
XX
SQ Sequence 707 BP; 199 A; 155 C; 178 G; 173 T; 0 U; 2 Other;
Query Match 20.2%; Score 428.8; DB 3; Length 707;
Best Local Similarity 77.4%; Pred. No. 2.3e-96;
Matches 546; Conservative 1; Mismatches 149; Indels 9; Gaps 2;
QY 23 GCATTGTTCTTGTGCGCTTACTTTTGGCACTTGTGATCGGCGGCAATTTTCGGGTGACG 82
Db 1 GCATTGTTCTTGTGCGCTTACTTTTGGCACTTGTGATCGGCGGCAATTTTCGGGTGACG 60
QY 83 CTGTTGTCGATCAACGCGCGCGGTACCGGTCACCTTCAAGTCAAGACGTTCCCA 142
Db 61 CTGTTGTCGATCAACGCGCGCGGTACCGGTCACCTTCAAGTCAAGACGTTCCCA 120
QY 143 CTGCGCTTCTGCGGGTCTTCGCTAGAAACACACGCGGTCAACGACCCGCGGTG 202
Db 121 CTCGCGCTTCTGCGGGTCTTCGCTAGAAACACACGCGGTCAACGACCCGCGGTG 180
QY 203 CGGCAATCGGCTGTGAGACGGAATATTGCACTTCTGTAAGATGCAATGTTTC 262
Db 181 CGGCAATCGGCTGTGAGACGGAATATTGCTTCTTATAAACAAGACGTAACGAAATTC 240
QY 263 CAATAGCAACAACAGAGAAAGAGCTGCTGTTTAAAGAGAGATATCTGTTTAT 322
Db 241 CGGCAATCGGCTGTGAGACGGAATATTGCTTCTTATAAACAAGACGTAACGAAATTC 300
QY 323 ACGGTTCCAAAAAGATCAACGCTCAGCAGCTTAAAGATATAAATTCGTCAACCAATCC 382
Db 301 ACGGTTCCAAAAAGATCAACGCTCAGCAGCTTAAAGATATAAATTCGTCAACCAATCC 360
QY 383 CGGCAATCGGCTGTGAGACGGAATATTGCTTCTTATAAACAAGACGTAACGAAATTC 442
Db 361 ATGTGAGGTTTATCATCGGAGGAGGAGTCTCCGCTTAAAGAGAGATATCTGTTTAT 420
QY 443 CAGGTTATGATATATAAGACGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 496
Db 421 CAGGTTATGATATATAAGACGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 497 ACAAGCAGTCTACCAACCGGTTTGTGATGACGGTTTGTATATATTCGGAGACATC 556
Db 481 GTRAGAGTTTGTATACCGGTTTGTGATGACGGTTTGTATATATTCGGAGACATC 540
QY 557 CTTTCGCAATCTTTTACGAGCGCGGGAACCGGTGAATATTCGCGCACTGCAATATATGA 616
Db 541 CTTTCGCAATCTTTTACGAGCGCGGGAACCGGTGAATATTCGCGCACTGCAATATATGA 600
QY 617 CCGATGCAATCTTTTACGAGCGCGGGAACCGGTGAATATTCGCGCACTGCAATATATGA 676
Db 601 CCGATGCAATCTTTTACGAGCGCGGGAACCGGTGAATATTCGCGCACTGCAATATATGA 657
QY 677 TCGTTTATATGAGTCAAAATGTCGGAGCAACTTCTTATGCTGGA 721
Db 658 CCAATATATGAGTCAAAATGTCGGAGCAACTTCTTATGAGCTA 702

RESULT 13
ABS67377 standard; DNA; 3300 BP.
ID ABS67377 standard; DNA; 3300 BP.
XX
AC ABS67377;
XX
DT 29-NOV-2002 (first entry)
XX
DE Neisseria gonorrhoeae lbpA gene.
XX
KW Gram-negative bacterial bleb; PorB; outer membrane protein;
KW Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
KW protective antigen; antibacterial; vaccine; gene; ds.
XX
OS Neisseria gonorrhoeae.
XX
FN WO200262380-A2.
XX
PD 15-AUG-2002.
XX
DF 08-FEB-2002; 2002WO-EP001356.
XX
PR 08-FEB-2001; 2001GB-00003169.
XX
PA (SMIX) SMITHLINE BEECHAM BIOLOGICALS.
XX
PI Berthet FJ, Lobet Y, Poolman J, Verlant VGCL;
XX
DR WPI; 2002-657510/70.
DR P-PSDB; ABG31056.
XX
PT Novel gram-negative bacterial bleb presenting on its surface PorB outer
PT membrane protein from Chlamydia trachomatis or protective antigen from
PT Chlamydia pneumoniae, useful for preventing Chlamydia infection.
XX
PS Disclosure; Page 48-49; 75pp; English.
XX
CC The present invention relates to a new gram-negative bacterial bleb
CC presenting on its surface the PorB outer membrane protein from Chlamydia
CC trachomatis, or a protective antigen from C. pneumoniae. The invention is
CC useful for preventing C. trachomatis or C. pneumoniae infection in a
CC host. The present nucleic acid sequence represents a Neisseria
CC gonorrhoeae gene as described in the invention
XX
SQ Sequence 3300 BP; 897 A; 807 C; 921 G; 675 T; 0 U; 0 Other;
Query Match 4.9%; Score 104.6; DB 6; Length 3300;
Best Local Similarity 74.9%; Pred. No. 2e-15;
Matches 131; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 1931 CTCGGGAGAACGTAATGACCTTCTGCGGAGGTTTCGACTAACCCGAGAACTTCAAG 1990
Db 1 CTCGGGATACGCAATCAATCTTTCGGGAAATGTTTCGACTAATCTCAAGTTTCAAG 60
QY 1991 CCGCAATCTTCTGTAACAGCGGCTTTTATGCGCGGAGGAGATTCGGCGGTA 2050
Db 61 CCGCAATCTTCTGTAACAGCGGCTTTTATGCGCGGAGGAGATTCGGCGGTA 120
QY 2051 ATATTATCGACGAGCCGCAATTCGGTCCGTTATTCGGCGGAGGAGATGA 2105
Db 121 CTATTTTCAATAGGATGGGAATCTCTTGGTATACTGAAGATATTTGAAGATGA 175
RESULT 14
AAS69547
ID AAS69547 standard; cDNA; 708 BP.
XX
AC AAS69547;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #5351.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 12:38:10 ; Search time 154.323 Seconds
(without alignments)
7637.968 Million cell updates/sec

Title: US-10-735-098-9
Perfect score: 2124
Sequence: 1 atgtgtaaacgcaattatgg.....acaaggaggaacacgatga 2124

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	86.2	4.1	7218	1	US-08-232-463-14
C 2	86	4.0	929	4	US-09-671-317-14
C 3	86	4.0	1001	4	US-09-671-317-14
C 4	79.8	3.8	43795	3	US-08-742-185-101
C 5	75.8	3.6	2223	1	US-08-257-073-4
C 6	74.8	3.5	3211	2	US-08-574-959A-8
C 7	74.8	3.5	3211	2	US-09-357-014-8
C 8	74.8	3.5	3901	2	US-08-574-959A-6
C 9	74.8	3.5	3901	3	US-09-357-014-6
C 10	74.4	3.5	16442	3	US-08-781-891-208
C 11	74.4	3.5	16442	4	US-09-618-166-208
C 12	71.4	3.4	390	3	US-09-197-649-7
C 13	69.4	3.3	1276	3	US-09-177-325-2
C 14	69.4	3.3	1276	3	US-09-411-812A-2
C 15	69.4	3.3	1276	4	US-09-590-113-2
C 16	69.2	3.3	3337	1	US-08-072-610-1
C 17	69.2	3.3	3337	2	US-08-719-822B-1
C 18	69.2	3.3	3337	3	US-09-092-458-1
C 19	68.4	3.2	366	2	US-08-766-738-2
C 20	68.4	3.2	966	4	US-09-262-610-2
C 21	67.2	3.2	1236	2	US-08-741-134-5
C 22	65.4	3.1	5394	3	US-08-688-376-1
C 23	65	3.1	3489	4	US-08-728-323A-1
C 24	65	3.1	3489	4	US-09-298-568-1
C 25	65	3.1	3489	4	US-09-410-399-1
C 26	65	3.1	32207	3	US-08-770-379-20
C 27	65	3.1	32207	3	US-08-757-669A-20

C 28	65	3.1	32207	4	US-09-230-371A-20
C 29	64.8	3.1	2230	3	US-08-448-194-7
C 30	64.8	3.1	2230	4	US-08-867-921-7
C 31	64.4	3.0	2106	3	US-08-613-009A-4
C 32	64.4	3.0	2106	4	US-08-778-570B-4
C 33	64.4	3.0	2106	4	US-09-059-584-4
C 34	64.4	3.0	2247	3	US-08-613-009A-3
C 35	64.4	3.0	2247	4	US-08-778-570B-3
C 36	64.4	3.0	2247	4	US-09-059-584-3
C 37	64.4	3.0	8266	4	US-09-059-584-54
C 38	62.8	3.0	3955	4	US-09-976-594-207
C 39	61.6	2.9	1052	1	US-08-466-603-1
C 40	61.6	2.9	1052	1	US-08-314-503A-1
C 41	61.6	2.9	1052	1	US-08-468-066-1
C 42	61.6	2.9	1052	2	US-08-466-717-1
C 43	61.6	2.9	1052	3	US-08-466-743-1
C 44	61.6	2.9	1052	5	PCT-US95-12414-1
C 45	61.2	2.9	2139	4	US-09-059-584-50

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463;
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHREIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Iardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 4.1%; Score 86.2; DB 1; Length 7218;

Best Local Similarity 4.0%; Pred. No. 2.7e-12;
Matches 16; Conservative 249; Mismatches 132; Indels 0; Gaps 0;
QY 1331 TTTTGGACCTATGAAACTCGGACGATATAAACCCGACCGCGGTCCAAACCGAAGG 1390
Db 1442 TTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1383
QY 1391 CGCAGGATGAAGGGGACGAGAGGGTGTAGCGGTTGATAACGGTAAAGAAGCAAG 1450
Db 1382 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1323
QY 1451 ACGAATCGCGGATGAAGAAGCACCAGGACGAGTGTAGAGATGAAGCAAGATG 1510
Db 1322 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1263
QY 1511 AAGACGAAGAAGAAATCGAAGAGAACTTGAAGAAGAGCTGAAGAGAAAGCCGAAG 1570
Db 1262 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1203
QY 1571 AAGAAATTCGCGCAGAGAAGGCAACGGCGGTTGAGGACGATCTGCCCACTCCGAAG 1630
Db 1202 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1143
QY 1631 CCTCTAAGCAGGACATCGACCTTTCTGAAAGGTATCCGACGCGGCAAGCCGACA 1690
Db 1142 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1083
QY 1691 TTCCAAAAACGACGCGCATATATACCGGCACCTG 1727
Db 1082 RRRRRRRRRRRRRRRATCGCAAGCTCCTCGACCTG 1046

QY 1380 CCAACCGAAGCGCAGGATGAAGAGGGGACGAGAGGGTGTAGCGGTTGATAACGTA 1439
Db 880 CCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 821
QY 1440 AGAAGCGAAGACGAAATCGCGGATGAAGAAAGCACCAGGACGAGTCTAGAGATGA 1499
Db 820 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
QY 1500 AGACGAGATGACAGACCAAGAA-GAATTCGAAGAAGAACCTGAAGAAGAGAGCTGAAGAGG 1558
Db 760 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
QY 1559 AAGAACCGGAGAGAGAAATTCGCGGACGAGAGAGCA 1594
Db 700 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665

Query Match 4.0%; Score 86; DB 4; Length 929;
Best Local Similarity 64.4%; Pred. No. 1.1e-12; Indels 1; Gaps 1;
Matches 139; Conservative 0; Mismatches 76; Indels 1; Gaps 1;
QY 1380 CCAACCGAAGCGCAGGATGAAGAGGGGACGAGAGGGTGTAGCGGTTGATAACGTA 1439
Db 880 CCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 821
QY 1440 AGAAGCGAAGACGAAATCGCGGATGAAGAAAGCACCAGGACGAGTCTAGAGATGA 1499
Db 820 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
QY 1500 AGACGAGATGACAGACCAAGAA-GAATTCGAAGAAGAACCTGAAGAAGAGAGCTGAAGAGG 1558
Db 760 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
QY 1559 AAGAACCGGAGAGAGAAATTCGCGGACGAGAGAGCA 1594
Db 700 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665

RESULT 3
US-09-671-317-439/c
Sequence 439 Application US/09671317
Patent No. 6528260
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US 09/671,317
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SOFTWARE: Patent.pm
SEQ ID NO 439
LENGTH: 1001
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-454-242 : deletion AT
NAME/KEY: misc.binding
LOCATION: 481..500
OTHER INFORMATION: 12-454-242.mis1, potential
NAME/KEY: primer_bind
LOCATION: 260..279
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 755..773
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc.feature
LOCATION: 795..800

OTHER INFORMATION: n=a, g, c or t
US-09-671-317-439

Query Match 4.0%; Score 86; DB 4; Length 1001;
Best Local Similarity 64.4%; Pred. No. 1.2e-12;
Matches 139; Conservative 0; Mismatches 76; Indels 1; Gaps 1;
QY 1380 CCAACCGAAGCGCAGGATGAAGAGGGGGACGAGGGGTGTAGGCGTTGATACCGTAA 1439
Db 1001 CCATCTCAAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 942
QY 1440 AGAAGCGAAGAGAAATCGCGGATGAAGAAAGCAACGGAGACGAACTGCTAGAGATGA 1499
Db 941 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 882
QY 1500 AGACGAGATGAAGACGAGAA-GAAATCGAAGAGAACTGAGAGAGAGAGAGAGAGAG 1558
Db 881 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 822
QY 1559 AAGAACCGAAGAGAAATTCGCGGACAGAGAGGCA 1594
Db 821 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786

RESULT 4

US-08-742-185-101
; Sequence 101, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DNA: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match 3.8%; Score 79.8; DB 3; Length 43795;
Best Local Similarity 64.2%; Pred. No. 3e-10;
Matches 120; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 1388 AGCGCAGGATGAAGAGGGGGACGAGGGGTGTAGGCGTTGATACCGTAAAGACG 1447
Db 38855 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 38914
QY 1448 AGACCAAAATCGCGGATGAAGAAAGCACCGGAGACGAACTGCTAGAGATGAAGACG 1507
Db 38915 AAGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 38974
QY 1508 ATGAACGACGAAGAGAAATCGAAGAGAAACCTGAAGAGAACTGAGAGAGAGAACCCG 1567
Db 38975 AAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1594
QY 1568 AAGAAGA 1574
Db 39035 AAGAAGA 39041

RESULT 5

US-08-257-073-4
; Sequence 4, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2570
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-073-4

Query Match 3.6%; Score 75.8; DB 1; Length 2223;
Best Local Similarity 58.0%; Pred. No. 7.7e-10;
Matches 134; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1357 ATAAAAACCGAAGCCCGCGGTCACCAAGCGCGAGGATGAAGAGGCGAAGAG 1416
DB 1984 ATAGAAGCTGAAGTGGATGCCCTCGCACCAAAATTAAGGAAGGAAGAAAAGAAA 2043

QY 1417 GGTGTAGCGTGTGATAACGGTAAAGAAAGCAAGCAAAATCGCGGATGAAGAAAGCACC 1476
DB 2044 GAAAAAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAA 2103

QY 1477 GGACAGCAAGTCTGTAGAGATGAAGACGAAGATGAAGACGAAGAAATCGAAGAGAA 1536
DB 2104 AAGAAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAA 2163

QY 1537 CCTGAAGAGAACTGTAGAGAGAGAAACCCGCAAGAAATTCGCGGAGAA 1587
DB 2164 CAAGAAGAAGAAGAAGAAATAGTACCGAGAAATTTGACACTGAAGAA 2214

QY 1454 AAATCGCGCATGAAGAAAGCACCAGAGACGAAGTCTGTAGAAAGATGAAGACGAAGATGAAG 1513
DB 2483 AGAAGAGCTTTGAGGAAGAGAGAGATGAAGAGGAATATTTTGAAGAGGAAGAGAGG 2542

QY 1514 ACGAAGAGAAATCGAAGAAAGAACCTGAAGAAAGCTGAAGAGGAAGAACCCGCAAGAG 1573
DB 2543 AGGAAGAAGAGTTTGAAGGAAGAAATTTGAGGAAGGAAGAGGTGAGTTAGGAAGAGAG 2602

QY 1574 AATGCCCGCAGAGAGAG 1591
DB 2603 AAGAGGAGGATGAGGAGG 2620

RESULT 7
US-09-357-014-8
; Sequence 8, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Jyoung, Ratna K. Vadlamudi
; and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/357,014
; FILING DATE: 19-Jul-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/574,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8

Query Match 3.5%; Score 74.8; DB 3; Length 3211;
Best Local Similarity 61.1%; Pred. No. 1.7e-09;
Matches 121; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1394 AGATGAAGAGCGGCGAGAGGGTGTAGCGTTGATAACGGTAAAGAAAGCGAAGACG 1453
DB 2423 AGGAAGAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGG 2482

QY 1454 AAATCGCGCATGAAGAAAGCACCAGAGACGAAGTCTGTAGAAAGATGAAGACGAAGATGAAG 1513
DB 2483 AGGAAGACTTTGAGGAGAGGAGGAGGATGAAGAGGAATATTTTGAAGAGGAAGAGG 2542

RESULT 6
US-08-574-959A-8
; Sequence 8, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Jyoung, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
US-08-574-959A-8

Query Match 3.5%; Score 74.8; DB 2; Length 3211;
Best Local Similarity 61.1%; Pred. No. 1.7e-09;
Matches 121; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1394 AGGATGAAGAGCGGCGAGAGGGTGTAGCGTTGATAACGGTAAAGAAAGCGAAGACG 1453
DB 2423 AGGAAGAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGG 2482


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RESULT 12
US-09-197-649-7
, Sequence 7, Application US/09197649
, Patent No. 6194550
, GENERAL INFORMATION:
, APPLICANT: Gold, Larry
, APPLICANT: Tuerk, Craig
, APPLICANT: Pribnow, David
, APPLICANT: Smith, Jonathan D.
, TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
, FILE REFERENCE: NEX02/C1-CON
, CURRENT APPLICATION NUMBER: US/09/197,649
, CURRENT FILING DATE: 1998-11-23
, EARLIER APPLICATION NUMBER: 07/829,461
, EARLIER FILING DATE: 1992-01-31
, EARLIER APPLICATION NUMBER: 07/739,055
, EARLIER FILING DATE: 1991-08-01
, EARLIER APPLICATION NUMBER: 07/561,968

```

Patent No. 6090620

GENERAL INFORMATION:

APPLICANT: Fu, Ying-Hui

APPLICANT: Yu, Chang-En

APPLICANT: Oshima, Junko

APPLICANT: Mulligan, John T.

APPLICANT: Schellenberg, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO WERNER'S SYNDROME

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,891

FILING DATE: 27-DEC-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: No. 6090620tenburg Ph.D., Carol

REGISTRATION NUMBER: 39,317

REFERENCE/DOCKET NUMBER: 240052.419

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 208:

SEQUENCE CHARACTERISTICS:

LENGTH: 16442 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-781-891-208

Query Match 3.5%; Score 74.4; DB 3; Length 16442;

Best Local Similarity 65.1%; Pred. No. 4.7e-09;

Matches 125; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 1386 GAAGGCGCAGGTATGAAGAGGGGCACGACAGGGTGTAGCGCTTGATAACGGTAAGAAGAAAG 1445

DB 16298 GCGAGGACGAGGAGGAGGACGAGCA-GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16240

QY 1446 CGAAGACGAATCCGGCATGAAGAACACCGGACACCAAGTCCTAGAAAGATGAAGACGA 1505

DB 16239 AGCAGCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16180

QY 1506 AGATGAAGACGAGAGGAAGAATCCAAGAAGAACTCCAAGAAGAACTGAAGAGGAGGAACC 1565

DB 16179 AGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 16120

QY 1566 CGAAGAAGAATT 1577

DB 16119 AGAAGAAGAAT 16108

RESULT 11

US-09-618-166-208/c

; Sequence 208, Application US/09618166

; Patent No. 6583112

GENERAL INFORMATION:

APPLICANT: Fu, Ying-Hui

APPLICANT: Yu, Chang-En

APPLICANT: Oshima, Junko

APPLICANT: Mulligan, John T.

APPLICANT: Schellenberg, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 23:48:06 ; Search time 1069.14 Seconds
(without alignments)
9777.159 Million cell updates/sec

Title: US-10-735-098-9
Perfect score: 2124

Sequence: 1 atgtgtaaacccaattatgg.....acaaggaggcaacacgatga 2124

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2124	100.0	2124	17	US-10-735-098-9
2	1562.4	73.6	2169	17	US-10-735-098-3
3	1516.8	71.4	2226	13	US-10-282-122A-29815
4	1499.8	70.6	2226	17	US-10-735-098-5
5	1296.2	61.0	2277	17	US-10-735-098-1
6	1291.8	60.8	2262	17	US-10-735-098-7
7	497.6	23.4	1000	17	US-10-343-561-15
8	104.6	4.9	3300	17	US-10-467-534-80
9	98.4	4.6	374849	13	US-10-087-192-1627
10	97.2	4.6	31124	13	US-10-087-192-463
11	96.6	4.5	37265	13	US-10-087-192-49
12	96	4.5	115223	17	US-10-322-281-773
13	95.4	4.5	635	13	US-10-027-632-269927
14	95.4	4.5	635	16	US-10-027-632-269927

C 15	93.8	4.4	305	9	US-09-864-761-19262	Sequence 19262, A
C 16	93.8	4.4	496	9	US-09-864-761-2534	Sequence 2534, Ap
C 17	93.6	4.4	96602	16	US-10-085-117-61	Sequence 61, Appl
C 18	90.6	4.3	39443	16	US-10-085-117-313	Sequence 313, App
C 19	90.2	4.2	276	9	US-09-864-761-20595	Sequence 20595, A
C 20	89.6	4.2	32069	15	US-10-004-113-7	Sequence 7, Appli
C 21	89	4.2	48652	13	US-10-087-192-859	Sequence 859, App
C 22	88.6	4.2	96596	12	US-10-052-482-70	Sequence 70, Appl
C 23	88.6	4.2	96597	12	US-10-052-482-103	Sequence 103, App
C 24	88.4	4.2	522	14	US-10-101-487-71	Sequence 71, Appl
C 25	88.4	4.2	530	14	US-10-101-487-73	Sequence 73, Appl
C 26	88.4	4.2	554	14	US-10-101-487-69	Sequence 69, Appl
C 27	88.4	4.2	554	14	US-10-101-487-106	Sequence 106, App
C 28	88	4.1	54786	12	US-10-052-482-211	Sequence 211, App
C 29	87.2	4.1	225883	15	US-10-175-523-57	Sequence 57, Appl
C 30	86.2	4.1	193853	13	US-10-087-192-1663	Sequence 1663, Ap
C 31	86	4.0	929	13	US-10-087-192-289	Sequence 289, App
C 32	86	4.0	1001	13	US-10-294-934-14	Sequence 14, Appl
C 33	86	4.0	143899	10	US-09-972-546-15	Sequence 439, App
C 34	85.6	4.0	4316	9	US-09-880-107-3713	Sequence 15, Appl
C 35	85.6	4.0	4316	13	US-10-257-021-81	Sequence 3713, Ap
C 36	85	4.0	559	9	US-09-864-761-7684	Sequence 81, Appl
C 37	85	4.0	210528	13	US-10-087-192-289	Sequence 7684, Ap
C 38	84.2	4.0	648	12	US-10-152-319A-2106	Sequence 2106, Ap
C 39	84	4.0	286	15	US-10-029-386-18943	Sequence 18943, A
C 40	84	4.0	577	15	US-10-029-386-5187	Sequence 5187, Ap
C 41	84	4.0	138115	17	US-10-322-281-377	Sequence 377, App
C 42	83.6	3.9	536	15	US-10-029-386-19974	Sequence 19974, A
C 43	83.6	3.9	599	15	US-10-029-386-6243	Sequence 6243, Ap
C 44	83.6	3.9	33454	13	US-10-087-192-1111	Sequence 1111, Ap
C 45	83.2	3.9	6944	15	US-10-172-086-111	Sequence 111, App

ALIGNMENTS

RESULT 1

US-10-735-098-9
; Sequence 9, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain 881607
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(2121)
US-10-735-098-9

Query Match 100.0%; Score 2124; DB 17; Length 2124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGTGTAAACCGAATATATCGCGCATTTGCTTGTTCCTTACTTTGGCATCTTCATC 60

1141 GATTCTCTAAAAATTTCCGTTGACGAGCGAAGTGGTGAATAATCCCGACCGTTTGGAGTT 1200
1141 GATTCTCTAAAAATTTCCGTTGACGAGCGAAGTGGTGAATAATCCCGACCGTTTGGAGTT 1200
1201 TCGATATGCGCGATTTTGGTTCATCCCGACAAATCTTGTGCGAAGCGCGTGAATTCCT 1260
1201 TCGATATGCGCGATTTTGGTTCATCCCGACAAATCTTGTGCGAAGCGCGTGAATTCCT 1260
1261 TTGCTAAACAAAGAAACAAATCCATCGATCTTCCGACGCGCAGGAAATGACCGTCCGTCT 1320
1261 TTGCTAAACAAAGAAACAAATCCATCGATCTTCCGACGCGCAGGAAATGACCGTCCGTCT 1320
1321 TGTTCGCACTTTTGAACCTATGTGAACCTCGACGATGAAGAAAGCAACGAGTCTGTAAGATGAA 1440
1321 TGTTCGCACTTTTGAACCTATGTGAACCTCGACGATGAAGAAAGCAACGAGTCTGTAAGATGAA 1440
1381 CAACGAGGCGCAGGATGAAGAGGGGACGAGAGGGGTGTAGGGCTGTGATAACCGGTAAA 1500
1381 CAACGAGGCGCAGGATGAAGAGGGGACGAGAGGGGTGTAGGGCTGTGATAACCGGTAAA 1500
1441 GAAAGCGAAGACGAAATCGGCGATGAAGAAAGCAACGAGTCTGTAAGATGAA 1560
1441 GAAAGCGAAGACGAAATCGGCGATGAAGAAAGCAACGAGTCTGTAAGATGAA 1560
1501 GACGAGATGAAGACGAAAGAAATCGAAGAGAACTCGAAGAGAACTGAGAGGAA 1620
1501 GACGAGATGAAGACGAAAGAAATCGAAGAGAACTCGAAGAGAACTGAGAGGAA 1620
1561 GAAACCGAAGAGAAATTCGCGCAGAGAAAGCAACGCGGTTCAGGCGAGCATCTCTGCC 1680
1561 GAAACCGAAGAGAAATTCGCGCAGAGAAAGCAACGCGGTTCAGGCGAGCATCTCTGCC 1680
1621 ACTCCGAGAGCTCTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATTCGACGCGG 1740
1621 ACTCCGAGAGCTCTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATTCGACGCGG 1740
1681 GAAAGCGAATTCGAAAGAAACGAGCGGCAATTAACCGGCACTTGGGAAGCGCGTATC 1800
1681 GAAAGCGAATTCGAAAGAAACGAGCGGCAATTAACCGGCACTTGGGAAGCGCGTATC 1800
1741 GCGGTATCGGATAGTGGTACGTCCTTCAAGAGGATAGCTATCGGAATCAAGGGGCAAAA 1860
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1801 GCAGAAATTTACCGTTGATTTGAAAGCGAAGACGCGTTCGGAATCTGACAGAAAAAAT 1920
1801 GCAGAAATTTACCGTTGATTTGAAAGCGAAGACGCGTTCGGAATCTGACAGAAAAAAT 1920
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1861 GATACAAACCCCGCTTTTATATGAAAGAGGTGATGACGCTAACCGTTCACCGCT 1980
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2041 TTGGGCGGTAAATATATGACAGCGAGGAAATTCGCTGGGTATTTGGGGCGAAAAA 2160
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RESULT 2
US-10-735-098-3
; Sequence 3, Application US/10735098
; Publication No. US20040131634A1

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121 TTCAGTCTAAGAGAGTTCCCACTTCGCTCTCTCGCGGTCTTCGCTAGAAACACGCGG 180
181 GTCACGACCGCGCTTGGTGGCGCAATGCGGCTGTGAGACGGAATATTGCAACTTCT 240
181 GTCACGACCGCGCTTGGTGGCGCAATGCGGCTGTGAGACGGAATATTGCAACTTCT 240
241 GATAAGGATGCAATGATTTTCCAAATAGCAAAACGAGGAAAGCTGTGCTTTAAA 300
241 GATAAGGATGCAATGATTTTCCAAATAGCAAAACGAGGAAAGCTGTGCTTTAAA 300
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361 AAAATTCGTCAACCAATCTTACGCGCAAGCAATTAACCAATCGGAAAGAAAAA 420
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421 TATGATTAATAATTTGTAGATGAGGTTATGATATATCTAAAGACGGAAGATGAAAT 480
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481 GAGTGGACTTCAAAATTAACAGCAGTCTCAACCGGTTTGGTTATGACGGTTTGTATAT 540
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1021 CGGTTTATCAGCAACGACAGAGCTATTCGCGCTGTTCGAGGCAACAAAAACAGAG 1080
1081 ACAGCAAAACGCAATCAGATACAAATCTGCGCTTGGCTTGAAGAACACCAAAATCTTG 1140
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: GENERAL INFORMATION:
: APPLICANT: Pettersson-Fernholm, Annika Margareta
: APPLICANT: Tommassen, Johannes Petrus Maria
: TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
: FILE REFERENCE: B45106C1
: CURRENT APPLICATION NUMBER: US/10/735,098
: CURRENT FILING DATE: 2003-12-12
: PRIOR APPLICATION NUMBER: 09/485,760
: PRIOR FILING DATE: 2000-02-15
: PRIOR APPLICATION NUMBER: PCT/EP98/05117
: PRIOR FILING DATE: 1998-08-10
: PRIOR APPLICATION NUMBER: GB 9717423.9
: PRIOR FILING DATE: 1997-08-15
: PRIOR APPLICATION NUMBER: GB 9805544.8
: PRIOR FILING DATE: 1998-02-05
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 2169
: TYPE: DNA
: ORGANISM: Neisseria meningitidis strain M981
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(2166)
US-10-735-098-3

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Query Match	73.6%;	Score 1562.4;	DB 17;	Length 2169;
Best Local Similarity	84.5%;	Pred. No. 0;		

Matches 1835;	Conservative	0;	Mismatches	286;	Indels	51;	Gaps	5;
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Db	1	ATGTGTAACCGAAATTA	TGGCGGCATTTGCT	TGTGTCCTTAC	TTTGGGCATCTT	TGCATC	60	
QY	61	GGCGGCAAATTTGGCGGTGC	AGCTGTGTCGAAATCA	ACGCGACCGCGTAC	CCCGTCACT	120		
Db	61	GGCGGCAAATTTGGCGGTGC	AGCTGTGTCGAAATCA	ACGCGACCGCGTAC	CCCGTCACT	120		
QY	121	TTCAAGTCTAAGGACGTTTCC	ACATTCGCTCTCGCGGTCT	TCGGTAGAAAC	CACCGCG	180		
Db	121	TTCAAGTCTAAGGACGTTTCC	ACATTCGCTCTCGCGGTCT	TCGGTAGAAAC	CACCGCG	180		
QY	181	GTCACACGACCGCGCTTGGT	TGCGGCAATGCGGCTGT	TGAGCGGAATAT	TGCAACTTCT	240		
Db	181	GTCACACGACCGCGCTTGGT	TGCGGCAATGCGGCTGT	TGAGCGGAATAT	TGCAACTTCT	240		
QY	241	GATTAAGCATGCGCAATGAT	TTTCCAAATAGCAAA	CAAGCAGAGAAAGCT	TGTCGTTTAAA	300		
Db	241	CGTGAAGATGGCAGCGCAAT	TCCCGATAGCAAA	CAAGCAGAGAAAGCT	TGTCGTTTAAA	300		
QY	301	GAGGAAATATCTGTGTTTTAT	ACGTTTCCAAAAGAGATCA	AGCTCAGCAGCTT	TAAGAT	360		
Db	301	GAAAGTGAATGTTCTGTGTTTTAT	ACGTTTCCAAAAGAGATCA	AGCTCAGCAGCTT	TAAGAT	360		
QY	361	AAAATTGCTCAACCAATCTT	ACGGCAAGCATTTACCACAT	TCGAAAAGAAAAATA	AAAAAA	420		
Db	361	GAAATTCATAAACGTAATCT	CTGAGGCAAGCATTTACCACAT	TCGAAAAGAAAAATA	AAAAAA	420		
QY	421	TATGATTATAAAATTTGT	TAGATCAGGTTATGTA	TATATATAAGACGGA	AAAGATGAAAT	480		
Db	421	TATAATATACGTTTGT	CTAGTCCCGTTATGTTT	TACTAAAAACGGA	AAAGATGAAAT	480		
QY	481	GAGTGCATTCAAATTAAC	AGCAGTCTACCAACCGGTT	TGCTTATGACGGTTT	TGTTATAT	540		
Db	481	GAGAAAACATCGGATGAA	AAAGCAGTTTCTAATCGTT	TTAGGCTATGACGGTT	TTTGTAAT	540		
QY	541	TATTCGGAGACATCC	TTTCGCAATCTTTAC	CGAGCGGGGAACCGGT	TGAAATATTTCCGGC	600		
Db	541	TATTCGGAGACATCC	TTTCGCAATCTTTAC	CGAGCGGGGAACCGGT	TGAAATATTTCCGGC	600		
QY	601	AAC TGCGCAATATAT	GACCATGCCATACGT	TCATCGAACGGA	AAAGCAGGAGATC	CTTAGC	660	
Db	601	AAC TGCGCAATATAT	GACCATGCCATACGT	TCATCGAGAGGTAA	--GGGGTTTCCAGT	657		

QY	661	GAAGATTGGGTTATATCGTTTATTACGGTCAAAAATGTCGAGCAAACTCTTATGCTGCG	720
Db	658	GTGGATTGGGTTATACCAATATATGGTAAATGGGACGCTTCTTATGAGGCT	717
QY	721	ACTGCCACACCGGAGGGAAACAATCTCGCGAATATACGGTTAAATTCGACCAAAAA	780
Db	718	AGGATGCCGATGCGCGGAAAAACATCTCTGCCAATAACGGTTAAATTCGCAAAAAA	777
QY	781	ACTCTGAATGGCAAGCTGATTAAAAATCAGTATGTGCRAAGAGAGATGATCCTAAAAA	840
Db	778	AACCTGGAGGTAAGTTGATTAAAAATCAGTATGTGCRAAGAGAGATGATCCTAAAAA	837
QY	841	CCACTGACCATTTACGACATTACTGCAAAATTTGGACGGCAACCGCTTTTACGGCAGTCC	900
Db	838	CCACTGACCATTTACCAACATTACCGCAACATTTGHAOGCACCCTTTACGGCAGTCC	897
QY	901	AAAGTTAAACACGAGGTGAAGACGAATACGCTGATAAAGAATATTTGTTTTCCATACC	960
Db	898	AAAGTTAGCACCGAGGTGAAGACGAACACGCTGATAAAGAATATTTGTTTTCCATACC	957
QY	961	GATGCCGATCAGCGGCTTGAGCGCGGTTTTTTTGGCGATAGGGGAAGAGCTTGCCGGA	1020
Db	958	GATGCCGATCAGCGCTTGAGCGCGGTTTTTTTGGCGATAGGGGAAGAGCTTGCCGCG	1017
QY	1021	CGGTTTATCAGCAACGACACAGCGTATTCGCGCGTGTTCGCAGGCAAAACAAAAACAG	1080
Db	1018	CGGTTTATCAGTAAACGACACAGCGTATTCGCGCGTGTTCGCAGGCAAAACAAAAACAG	1077
QY	1081	ACAGCAAAACGATCAGATACAAATCTGCTGCTGCTGGAACAACACCAAAATCTTG	1140
Db	1078	ACAGCAAAACGATCAGATACAAATCTGCTGCTGCTGGAACAACACCAAAATCTTG	1137
QY	1141	GATTCCTCTAAAAATTTTCGTTGACGAGCAAGTGTGAAATCCCGACCGTTTGAGTT	1200
Db	1138	GATTCCTCTAAAAATTTTCGTTGACGAGCGACTGATGACCATGCGCGCTTAAGTTTGC	1197
QY	1201	TCCATATGCGCGATTTTGGTCTATCCGACAAAATCTTCTGTGCAAGGGCGTGAATTCCT	1260
Db	1198	TCCATATGCGCGATTTTGGTCTATCCGACAAAATCTTCTGTGCAAGGGCGTGAATTCCT	1257
QY	1261	TTGGTAAACAAGAACAAACCATCGATCTTGCAGACGCGAGGAAAATGACCGTCCGTCT	1320
Db	1258	TTGGTTAGCCAAAGAAACCAATCGACTTTCGCGACGCGAGGAAAATGACCATCCGTCT	1317
QY	1321	TGTTGCGACTTTTGACTATGTGAAACTCGACCGATTAACACCGAACGCGCGCTC	1380
Db	1318	TGTTGCGACTTTTGACTATGTGAAACTCGACCGATTAACACCGAACGCGCGCTC	1377
QY	1381	CAACGGAAGGCGAGGATGAAGAGGGGGAACGAAAGAGGTGTAGGCGTGTATACGTAAC	1440
Db	1378	AAACCGAAGGCGAGGATGAAGAGGATTCGGAATTTGATGTAATGCGGAAGAACGAGAC	1437
QY	1441	GAAC--GCCAAGACGAAATCGCGATGAAGAACCAACCGGAGA	1481
Db	1438	GAATTTCCGAAGATGATTAACCGCGAAGATGAAGTCAACGGAAGAGAGGAAGTGAAGA	1497
QY	1482	--CGAAGTCTGAAGATGAAGACGGAAGATGAAGACGGAAGAAATTCGCCGCGAGAAGGC	1593
Db	1498	ACCGAAGAGAAACTGATGAACGACGAGAGGAGAACCGGAAGAACTGAAGAAACTGAA	1557
QY	1534	GAACCTGAAGAGAGCTGAAGAGGAAGAACCGGAAGAAATTCGCCGCGAGAAGGC	1617
Db	1558	GAACCTGAAGAACTGAAGAACTGAAGAACTGAAGAAATTCGCCGCGAGAAGGC	1617
QY	1594	AACGGCGGTTACGGCAGCATCTGCCACTCGCGAAGCTCTTAAAGCAGGACATCGAC	1653
Db	1618	AACGGCGGTTACGGCAGCATCTGCCACTCGCGAAGCTCTTAAAGCAGGACATCGAC	1677
QY	1654	CTTTTCTGAAAGGTTATCGCACGCGGAAGCCGACATTTCCAAAAACGGAACGGCGAT	1713
Db	1678	CTTTTCTGAAAGGTTATCGCACGCGGAAGCCGACATTCGCAAAATGGAAGACGACGC	1737


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QY 901 AAAGTTAAACACAGAGGTGAAGACGAATCACGCTGATAAGAAATATTTCTTTTCCATACC 960
Db 901 AAAGTTAAACACCGAGGTGAAGACGAACACGCTGATAAGAGCAATTTGTTTTCCATACC 960
QY 961 GATCCGATCAGCGCGCTTGAGGCGGTTTTTTTCGCGGATAAGGGGAGAGCTTGCCGGA 1020
Db 961 GATCCGATCAGCGCGCTTGAGGCGGTTTTTTTCGCGGATAAGGGGAGAGCTTGCCGGA 1020
QY 1021 CGGTTTATCAGCAACAGCAAGCTATTCGGCGTTCGAGGCAACAAAAACAGAG 1080
Db 1021 CGGTTTATCAGCAACAGCAAGCTATTCGGCGTTCGAGGCAACAAAAACAGAG 1080
QY 1081 ACAGCAACGATCAGATACAAATCTCGCGCTCTGAAACACACCAAAATCTTG 1140
Db 1081 GCATCAACGATCAGATACAAATCTCGCGCTCTGAAACACACCAAAATCTTG 1140
QY 1141 GATTTCTTAAATTTCCGTGTGACGAGCAAGTGGTGAATCCCGACCGTTTGAGTT 1200
Db 1141 GATTTCTTAAATTTCCGTGTGACGAGCAAGTGGTGAATCCCGACCGTTTGAGTT 1200
QY 1201 TCCACTATGCCGATTTTGGTCAATCCGACAACTTCTTGTGAGGGGTGAATTCCT 1260
Db 1201 TCCCTATGCCGATTTTGGTCAATCCGACAACTTCTTGTGAGGGGTGAATTCCT 1260
QY 1261 TTGGTAAACAAAGAAACAAACCAATCTGCTGCGACGCGAGGAAATGACCGTCCGTGCT 1320
Db 1261 TTGGTCAAAAGATCTCAAAACCAATCTGCTGCGACGCGAGGAAATGACCGTCCGTGCT 1320
QY 1321 TCGTGGACCTTTTGGCTATGTGAACTCGACCGATATAAACCGAACCGCCCGCGCTC 1380
Db 1321 TCGTGGACCTTTTGGCTATGTGAACTCGACCGATATAAACCGAACCGCCCGCGCTC 1380
QY 1381 CAAACGAGCGCGAGATCAAGAGGGGACGAGAGGGGTGTAGGC----- 1425
Db 1381 AAAAAAGGCGAGATGAAATTTCCGAAGATGAAATTTGGTGAAGCGAGGAAATGAA 1440
QY 1426 -----GTTGATAACGGTAAAGAAAGCGAAGACGAAATCGCGATGAAAGACACC 1476
Db 1441 GAGGATTTGGTGGCTGAAGAGAAACACGAGAGAGAGTCTGTAAGATGAAGACAGA 1500
QY 1477 GGAGACGAGTCTGTAGATGAAGACGAGATGAAGACGAGAGAGAAATCGAAGAGAA 1536
Db 1501 GAAGAAGACGAGTTCGGAAGATGTTAAGACGAGTGAAGACGAGAGAAATCGCGAAGAA 1560
QY 1537 CCTGAAGAGAGCTGAAGAG-----GAAGAACCGAAGAGAAATTCGCGCAGAA 1587
Db 1561 GATGATGATGAGCGAGAGAGAGAGTGAAGAACCGAAGAGAAATCGCGCAGAA 1620
QY 1588 GAAGCAACCGCGGTTGAGGACGATCTGCGCCACTCGCGAAGCTCTTAAGGCGAGGAC 1647
Db 1621 GCGCGCGTGGCGGTTGAGACGCGATCCGCGCGCTTCGAGAGCCCTTAAGGCGAGGAC 1680
QY 1648 ATGACCTTTTCTGAAAGGTATCCGACGCGAAGCGACATTCGCAAAACCGAAGC 1707
Db 1681 ATGACCTTTTCTGAAAGGTATCCGACGCGAAGCGACATTCGCAAACTGGAAGAA 1740
QY 1708 GCGCATATATACCGCACTTGGAGCGGCTATCGCGGTATCGGATGTGGTACGTCATT 1767
Db 1741 GCAGCTATACCGCACTTGGAGCGCGTATCAGC-----AAACCCATT 1785
QY 1768 CAAAAGATAGCTATGCAATCAA--GGGCAAAAGCAGAAATTTACGTTGATTTGAA 1824
Db 1786 CAATGGGATATAAGGCGGATATAAAGCGGCAAAAGCAGAAATTTGACGTTGATTTCCGC 1845
QY 1825 GCGNAGCGGTGTCGGAATGTGACAGAAAAAATGATACAAACCCCGCTTTTATATT 1884
Db 1846 GAGAAATCGAATTTCCGGAACGCTGACGAGAAAAAAGCTGTAGAGCTGCTTTCTATATT 1905
QY 1885 GAAAAAGGTGTGATTCAGCGTAACGCTTTCCACGCTTTGGCGCATACTCGGGAGAACG 1944
Db 1906 GAAAAAGGTGTGATTCAGCGTAACGCTTTCCACGCGACACGACGCTCGGGATACGGC 1965
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QY 1945 ATTGACCTTTCTGGCGAGGGTTGACTAAACCCGAGAACTTCAAGCCGCAATCTTCTT 2004
Db 1966 ATCAATCTTTCCGGAAATGGTTGACCAACCCCAAAACCTTCCAAAGCTAGTGATCTT 2025
QY 2005 GTAAACAGCGCGCTTTTAAGCCGCGAGCGGCGAGAAATGGGCGGTAAATATTATCGACAGC 2064
Db 2026 GTAAAGAGGAGATTTTACGGCCGCGACGCGAGGAAATGGGCGGTACTATTTTCAATAAG 2085
QY 2065 GACCGAAATTCGGTGGGTATTTGGGCGGAAAAAGATGACAAAGGAGC 2114
Db 2086 GATGGAAATCTCTTGATATACTGAAGATATTGACAATGAAATTTGAAGC 2135
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RESULT 4

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US-10-735-098-5
; Sequence 5, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2226
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain H44/76
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2223)
US-10-735-098-5
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Query Match 70.6%; Score 1499.8; DB 17; Length 2226;
Best Local Similarity 83.3%; Pred. No. 0;
Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;
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QY 1 ATGTGTAACCGAATTATGGCGCATTTGCTTTGTGGCCCTTACTTTTGGCATCTTGATC 60
Db 1 ATGTGTAACCGAATTATGGCGCATTTGCTTTGTGGCCCTTACTTTTGGCATCTTGATC 60
QY 61 GCGGCAATTTCCGCTGCGAGCTGTTGTGCAATCAACGCGCACCGGCTACCCGTCAC 120
Db 61 GCGGCAATTTCCGCTGCGAGCTGTTGTGCAATCAACGCGCACCGGCTACCCGTCAC 120
QY 121 TTCAAGTCTAAGACGCTTCCCACTTCGCTCTCCCGGCTTCGCGTAGAAGAACGACGCG 180
Db 121 TTCAAGTCTAAGACGCTTCCCACTTCGCTCTCCCGGCTTCGCGTAGAAGAACGACGCG 180
QY 181 GT-----CAACGACCGCGCTTGTGTCGGCAATCGGCTTTGAGACGGAATATGCA 234
Db 181 GTCCCGCTCAACCGGCGCTGCGCTGCGGCAATCGGCTTTGAGGCGGATTTGCGCA 240
QY 235 ACTTCTGATAAGATGCGAATGATTTTCAAAATAGCAAAACAGCAGAAAGAGCTGTGCG 294
Db 241 ACTTCTGATAAGATGCGAATGATTTTCAAAATAGCAAAACAGCAGAAAGAGCTGTGCG 300
QY 295 TTAAAGAGGAGATATCTGTTTATACGGTTCCAAAAAGATCAACGTCAGCAGCTT 354
Db 301 TTAAAGAGGAGATATCTGTTTATACGGTTCCAAAAAGATCAACGTCAGCAGCTT 360
QY 355 AAAGATAAAATTCGTCAACCAAAATCTACGCGCAAGCATTACCAATCGGAAGAAAT 414
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361	Db	AGGATATAAAATTCATCAACGCAATCTTAATGTAGAAATTTAGGACATATCAAGAAATGAAAT	420
415	Qy	AAAAATATGATTTATATAATTTGTAGATGACAGTTATGTATATCTAAAGACGGAAGAT	474
421	Db	AAAAAATATGGTTATGAAATTTTGGATGCGGTTATGTATATCTATAAAACGGAACAT	480
475	Qy	GAAATTTAGTGGACTTCAAAATTAACAAGCAGTCTACCAACCGGTTTGGTTATGACGGTTTT	534
481	Db	GAAATTTAGTGGACTTCAAAATCGAAGCAGTTTCTTAATCGTTTGGCTACGACGGTTTT	540
535	Qy	GTATATATTTCCGGAGAAACATCTCTTCGAAATCTTTTACCGAGCGCGGACGGTGAATAT	594
541	Db	GTATATATTTCCGGAGAAACATCTCTTCGAAATCTTTTACCGAGCGCGGACGGTGAATAT	600
595	Qy	TCCGGAACTGGCAATATATGACCGATGCGATACGTCATCGAAGAGAGAAAGCAGAGAT	654
601	Db	TCCGGTAACTGGCAATATATGACCGATGCGATACGTCATCGAAGAGAGAAAGCAGAGAT	660
655	Qy	CCTAGCGAAGATTTGGTTATATCGTTTATATACGTTCAAAATGTCGGAGCAACTCTTAT	714
661	Db	CCTAGCGAAGATTTGGTTATATCGTTTATATACGTTCAAAATGTCGGAGCAACTCTTAT	720
715	Qy	GCTCGCACTGCCAGACCGGAGGAAACATCTCCGAAATATACGGTTAATTTTCGAC	774
721	Db	GCTCGCACTGCCAGACCGGAGGAAACATCTCCGAAATATACGGTTAATTTTCGAT	780
775	Qy	CAAAAACTCTGAATGGCAAGCTGATTAATAAATCAGTATGTGCAAAAGAGAGATGATCT	834
781	Db	AAGAAACTTTGACGGTCAATTAATAAATCAGTATGTGCAAAAGAGAAACCGATGAA	840
835	Qy	AAAAAACCACTGACATTTACGACATTTGCAAAATTTGACGCGCAACCGCTTTTACCGGC	894
841	Db	AAGAAACCACTGACATTTACGACATTTGCAAAATTTGACGCGCAACCGCTTTTACCGGC	900
895	Qy	AGTGCCTAAAGTTAAACACAGAGGTGAAGACGAAATCACGCTGATAAAGAAATATTTGTTTC	954
901	Db	AGTGCCTAAAGTTAAACACAGAGTTGAAGACGAGCCAGCTGATAAAGAGCATTTGTTTTC	960
955	Qy	CATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTCGGCGATTAAGGGGAGAGCTT	1014
961	Db	CATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTCGGCGATTAAGGGGAGAGCTT	1020
1015	Qy	GCCGACGGTTTATCAGCAACGACACAGCTATTCGCGCTGTTTCGACGCAAAACAAAA	1074
1021	Db	GCCGACGGTTTATCAGCAACGACACAGCTATTCGCGCTGTTTCGACGCAAAACAAAA	1077
1075	Qy	ACAGACAGCAAAACGATCAGATCAAAATCTCGCTGCCCTCTGGAATAACACACCAAA	1134
1078	Db	ACAAACGATCAACGACGACATCAAAATCTCGCTGCCCTCTGGAATAACACACCAAA	1137
1135	Qy	ATCTTGGATCTCTAAAAATTTCCGTTGACGAGCAAGTGGTGAATAATCCCGACCGTTT	1194
1138	Db	ATCTTGGATCTCTGAAAAATTTCCGTTGACGAGGCGAGGATGAATAATCCCGACCGTTT	1197
1195	Qy	GAGTTTCCACTATGCCGATTTGGTCTATCCGCAAAATCTTTGTCAAGGGCGTGAA	1254
1198	Db	GCAATTTCCCTCTGCCGATTTGGTCTATCCGCAAAATCTTTGTCAAGGGCGTGAA	1257
1255	Qy	ATTCTTTGGTAAACAAAGAAACAAACATCGATCTTTCGCGACGCGGAAATGACCGTC	1314
1258	Db	ATTCTTTGGTAAACAAAGAAACCAATCGATCTTTCGCGACGCGGAAATGACCGTC	1317
1315	Qy	CGTGTGTTGGCACTTTTTCATCTATGTGAATCTCGACGGAATAAAACCGAACGCCC	1374
1318	Db	CGTGTGTTGGCACTTTTTCATCTATGTGAATCTCGACGGAATAAAACCGAACGCCC	1377
1375	Qy	GCGTCTCAACCGAGGCGCAGGATGAAGAGGGGAGCAAGAGGGTGTAGCGTTGATAC	1434
1378	Db	GCAAGTAAACCAAGGCGGAGATGAAGAGGGGATGAAGAGGGTGTAGCGTTGATAC	1437
1435	Qy	GGTAAAGACGGAAGACGAAATCGCGATGAAGAAAGCACCGGACGAAAGTCGTAGAA	1494
		1495 GATGAACGACGATGAAGACGAAAGAAATCGAAGAA-----GAACTGAA 1542	
		1498 GCGCATGAAGAGAGGTGCGAAGACGAAAGCCGCAAAACGAAAGCGCGGAAGAC 1557	
		1543 GAAGAAGCTGAAGAGGAGAAACCCGAAAGAAATTTCCGGCAGAGAGGCAACGCGGT 1602	
		1558 GAAGCTGAAGAAACCTGAAGAAACCCGAAAGAAATTCGCGCGCAGAGCGCGGTGGT 1617	
		1603 TCAGGACGATCTGCGCCACTCCGGAAGCCCTCTAAAGAGGAGGACATCGACCTTTCTG 1662	
		1618 TCAGACGCACTCTGCGCGCTCCGGAAGCTCCTAAAGCAGGATATCGACCTTTCTG 1677	
		1663 AAAGGTATCCGACGCGGAGGAGCAATTCGAAAGAAACGGAACGCGGCAATTAACCGGC 1722	
		1678 AAAGGTATCCGACGCGGAGGAGCAATTCGGAAGCGGCAATTCGAAAGAGCAATTAACCGGC 1737	
		1723 ACTTCGGAAGCGGATTCGGGTATCGGATAGTGTAAGTCTCAATTCGAAAGAGATGCTAT 1782	
		1738 ACTTCGGAAGCGGATTCGAC-----AAACCAATTCGAAAGAGATGCTAT 1782	
		1783 GCG---AATCAAGGGGCAAAAGCAGAAATTTACCGTTGATTTGGAAGCAAGCGGTGCC 1839	
		1783 GCGGATAAAAGACGCGCAAGACAAATTTGACGTTGATTTTCGCGCAGAAATCGATTC 1842	
		1840 GGAATGCTGACAGAAAAAATATACAAACCCCGCTTTTATATTTGAAAAAGGTGTGAT 1899	
		1843 GGAACGCTGACGAGAAAAACGTTGTACAACTCTTTTCCATTTTGAAGACGCGGTGAT 1902	
		1900 GACGTTAACGTTTTCACGCTTTGGCGCATCTCGGGAGAACGGTATTTGACCTTTCTGG 1959	
		1903 GAGGCAATTTGGTTTCCACGCGACAGCGCGCATCTGGGTAACGGCATCAATCTTTTCGGA 1962	
		1960 CAGGTTTTCGACTAACCCGGAAGAACTTTCAAAGCGCAATCTTTTGTGAACGCGGCTTT 2019	
		1963 AATGATTCGACTAATCTTCCAGTTTCAAAGCCAATATCTTCTTGTAAACGCGGCTTT 2022	
		2020 TATGCGCGGAGCGGCGCAATTTGGCGGTATATATTCGACAGCGACCGGAAATTCGGT 2079	
		2023 TACGCGCGGAGCGGAGAAATTTGGCGGTACTATTTTCAATATGATCGGAAATCTCT 2082	
		2080 GCGGTATTTGGGCGGAAAAAGATGACAAAGGCG 2114	
		2083 GGTATACTGAAGATCTGAAATGAAGCTGAAGC 2117	
		RESULT 5	
		US-10-735-098-1	
		; Sequence 1, Application US/10735098	
		; Publication No. US20040131634A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Pettersson-Fernholm, Annika Margareta	
		; APPLICANT: Tommassen, Johannes Petrus Maria	
		; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein	
		; FILE REFERENCE: B45106C1	
		; CURRENT APPLICATION NUMBER: US/10/735,098	
		; PRIOR FILING DATE: 2003-12-12	
		; PRIOR APPLICATION NUMBER: 09/485,760	
		; PRIOR FILING DATE: 2000-02-15	
		; PRIOR APPLICATION NUMBER: PCT/EP98/05117	
		; PRIOR FILING DATE: 1998-08-10	

; LOCATION: (100) ... (2274)
US-10-735-098-1

Query Match 61.0%; Score 1296.2; DB 17; Length 2277;
Best Local Similarity 79.0%; Pred. No. 0;
Matches 1672; Conservative 0; Mismatches 373; Indels 72; Gaps 8;

QY	1	ATGTGTAACCGAATTATGCGGCATTTGCTGTGCTCCCTTACTTTTGGCATCTTGATC	60
Db	100	ATGTGTAACCGAATTATGCGGCATTTGCTGTGCTCCCTTACTTTTGGCATCTTGATC	159
QY	61	GGCGGCATTTTCGGCGTGAGCTGTGTTCGAATCAACGCCAGCCGCTACCCGTCAC	120
Db	160	GGCGGCATTTTCGGCGTGAGCTGTGTTCGAATCAACGCCAGCCGCTACCCGTCAC	219
QY	121	TTCAAGTCTAAGGACGCTTCCCACTTCGCCTCTCGCGGCTCTTCGGTAGAACAACGCG	180
Db	220	TTCAAGTCTAAGGACGCTTCCCACTTCGCCTCTCGCGGCTCTTCGGTAGAACAACGCG	279
QY	181	GTCAACCGGACCGCGCTTGGTGGGGAATGCGGCTGTTGAGACGGAATATTGCAACTTCT	240
Db	280	GTCAACCGGACCGCGCTTGGTGGGGAATGCGGCTGTTGAGACGGAATATTGCAACTTCT	339
QY	241	GATTAAGATGGCAATGATTTTCCAAATAGCAACAAGCAGAAAGCAAGCTGTGCTTTAAA	300
Db	340	CGTGAAGATGGCAGCGAATTTCCAAATAGCAACAAGCAGAAAGCAAGCTGTGCTTTCAA	399
QY	301	GAGGAAGATATCGTGTGTTTTTATACGGTTCCAAAAAAGATCAACCTCAGCAGCTTAAAGAT	360
Db	400	GAGGTGATGTGCTGTGTTTTTATACGGTTCCAAAAAAGATCAACCTCAGCAGCTTAAAGAT	459
QY	361	AAAAATTCGTCAACCAAAATCTTACGCGCAGCAATTACCATCGGAAAGAAAAATAAAAA	420
Db	460	GAATTCATAACGTGATTCGATGTAGAAATAGGACATCAGAAAGGAAAAATAAAAA	519
QY	421	TATGATTTAAATTTGTAGATGCAAGCTGTATATATACTAAAGACGGAAGATGAAAT	480
Db	520	TATGATTTAAATTTGTAGATGCAAGCTGTATATATACTAAAGACGGAAGATGAAAT	576
QY	481	GAGTGGACTTCAAAATTACAAGCAGCTTACCAACCGGTTTGGTTATGACGGTTTGTATAT	540
Db	577	AAGTGGACTTCAAAATTACAAGCAGCTTACCAACCGGTTTGGTTATGACGGTTTGTATAT	636
QY	541	TATTCGCGAGAACATCTCTCGCAATCTTTACCAGCGCGGGAACGCTGAAATATTCGCG	600
Db	637	TATTCGCGAGAACATCTCTCGCAATCTTTACCAGCGCGGGAACGCTGAAATATTCGCG	696
QY	601	AACGCGCAATATGACCGATGCGATACGTCATCGAAACAGGAAAGCAGGAGATCCTAGC	660
Db	697	AACGCGCAATATGACCGATGCGATACGTCATCGAAACAGGAAAGCAGGAGATCCTAGC	753
QY	661	GAAGATTGGGTTATATCGTTTATACGGTCAAAATGTCGAGACCACTCTTATGCTGCG	720
Db	754	GACAAATTGGGTTATATCGTTTATACGGTCAAAATGTCGAGACCACTCTTATGCTGCG	813
QY	721	ACTGCCACCAACCGGAGGGAACAATCTTCGGAATATACGGTTTATGCGACCAAAA	780
Db	814	AAGATGTCACGAAAGGGGAAAAACATCTGCTTAAATATACGGTAGATTCGGTAAACAA	873
QY	781	ACTCTGAAATGGCAAGCTGATTTAAATATAGTATGTCGAAAGAGAGATGATCTTAAAAA	840
Db	874	ACCTGACCGCGAGCTGATTTAAACCAATATGTCGAAACCCAGGTGAGAAGC--AAAAA	930
QY	841	CCACTGACCAATTACGACATTTATGCAAAATTTGACGCGCAACCGCTTTTACCGGAGTGCC	900
Db	931	CCGCTGACCAATTACAAATCTGCGGATTTTAAACCGCAACCGCTTTTACCGGAGTGCC	990
QY	901	AAAGTTAAACACGAGGTGAAGCAATCAACGCTGATTAAGAAATATTTGTTTTTCCATACC	960
Db	991	AAGTCAATCTGATTTACGGAAGCCATGCAATTAAGGAGCATTTGTTTTTCCATGCC	1050
QY	961	GATGCGCATCAGCGGCTTGAGGCGGCTTTTTCGCGCATTAAGGGGAGAGCTTGCCGA	1020

Db		1051	GAATGCGCATCAGCGGCTTGAGGGCGGTTTTTTTCGGCGATAGGGGGAGAGCTTGGCCGA	1110
QY		1021	CGGTTTTATCAGCAACGACACACGGTATTTCGGCGTGTTCGAGGCAACAAAAACAGAG	1080
Db		1111	CGGTTTTATCAGCAACGACACACGGTATTTCGGCGTGTTCGAGGCAACAAAAACAGAG	1168
QY		1081	ACAGCAAAACGATCAGATACAAATCTGCCCTCTGGAACACACCAAAATCTTG	1140
Db		1169	-----CGTGCCCTCTGGAACACACCAAAATCTTG	1200
QY		1141	GAATTCCTATAAAATTTCCGTTGACGAGGCAAGTGTGAAAAATCCCGACCGTTTGAGGTT	1200
Db		1201	GAATTCCTGAAAAATTTCCGTTGATGAGGCAAGTGTGAAAAATCCCGACCGTTTGCCATT	1260
QY		1201	TCCACTATGCCGATTTTGGTTCATCCCGACAACTTCCTTGTGGAAGGGGTGAAATTCCT	1260
Db		1261	TCTCTATGCCGATTTTGGTTCATCCCGACAACTTCCTTGTGGAAGGGGTGAAATTCCT	1320
QY		1261	TGTTGTAACAAGAACCAACCATTCGTTGCGGCGGAGGAAATGACCGTTCAGTGTCT	1380
Db		1321	TGTTGTAACAAGAACCAACCATTCGTTGCGGCGGAGGAAATGACCGTTCAGTGTCT	1380
QY		1321	TGTTGCGACTTTTGCACCTATGTGAACCTCGGACGGAATAAAACCGCCCGCGCTC	1380
Db		1381	TGTTGCGACTTTTGCACCTATGTGAACCTCGGACGGAATAAAACCGCCCGCGCTC	1440
QY		1381	CAACCGAAGCGCAGGATGAAGAGGGGACGAAGAGGCTGTAGGCGTTGATACCGTAAA	1440
Db		1441	AAACCGAAGCGCA-----GACCGAAGAGGATTCGGAATTGATATGCGGAA	1488
QY		1441	GAAGCGAAGCGAAATTCGGCGATGAAGAAAGCACCGGAGACGAAGTCTGAGAAGTAA	1500
Db		1489	GAAGCGAAGCGAAATTCGGCGATGAAGAAAGCACCGGAGACGAAGTCTGAGAAGTAA	1548
QY		1501	GACGAAGATGAAGACGAGAGAAATCGAAGAGAACTGGAAGAAAGTGAAGAGGAA	1560
Db		1549	GAAGCGAAGAGAGAGAGAGGACCAAGAAACGAAGACGCGGAGAAAGACGAAGCTGAA	1608
QY		1561	GAACCGAAGAGAAATTCGGCGAGAGAAAGAGGCAACGCGGTTGAGGCGATCTCTGCC	1620
Db		1609	GAACCTGAAGAGAACTGTCGGC---AGAAGCGAACGCGAGTTCAAAGCGCATCTCTGCT	1665
QY		1621	ACTCCGGAGCTCTAAGACGAGGACATCGACTTTTCTGAAAGGTATCCGACACGGCG	1680
Db		1666	GTCCCGGAGCCTCTAAGACGAGGATTCGACTTTCTGAAAGGTATCCGACACGGCA	1725
QY		1681	GAAGCGCAATTCGAAAGAGCAACGGCGCATTTATACCGGCACTTGGGAAGCGGTATC	1740
Db		1726	GAACCGAATATCCGCAACTGGAAGACACGCTATACCGGCACTTGGGAAGCGGTATC	1785
QY		1741	GCGGTATCGGATAGTGGTTCATTCGAAAGGATAGCTATGCG---AATCAAGGGGCA	1797
Db		1786	GGC-----AAACCCATTCAATGGGCAATCATCGGATTAAGAGCGGCA	1830
QY		1798	AAAGCAGAAATTTACCGTTGATTTGAGCGAAGACGGTTCGGGAATGCTGACAGAAAA	1857
Db		1831	AAAGCAGATTTTACCGTTGATTTGCGGCAAGAAATCGATTTCGGAGCGCTGACGGAGAA	1890
QY		1858	AATGATACAAACCCCGCTTTTATATGAAAAGGTGCAATTCGGAATGCTGACAGAAAA	1917
Db		1891	AACGGTGTAGAACCTGCTTTCCGTTATGAAAACGGCGTATTTGAGGGCAACGGTTTCCAT	1950
QY		1918	GCTTTGGCGATATCCTGGGAGAACGGTATGACCTTTCTGGGACGGTTTCGACTAACCCG	1977
Db		1951	CGGACAGCGGCACTCGGGATGACGGCATTCGACCTTTCCGGGACGGTTTCGACCAACCG	2010
QY		1978	AAGAACTTCAAGCGCAATCTCTGTTATACAGCGCGCTTTTATGGCCCGCAGCGGCA	2037
Db		2011	CAGATCTTCAAGCTTAATGATCTTCGTGTAGAAGGAGGATTTTACGGCCGGAAGCGGAG	2070
QY		2038	GAATTTGGCGGTAAATATATTCGACAGCGACCGGAAATTCGGTGGTATTTGGGGGAAA	2097
Db		2071	GAATTTGGCGGTAAATATTTCAATTAATGATCGGAATCTCTTGGTATACTGAAGGTACT	2130

QY 2098 AAAGATGACAAAGGAGGC 2114
Db 2131 GAAATAAAGTTGAAGC 2147

RESULT 6
US-10-735-098-7
; Sequence 7, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tomassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M990
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2259)
US-10-735-098-7

Query Match 60.8%; Score 1291.8; DB 17; Length 2262;
Best Local Similarity 78.1%; Pred. No. 0;
Matches 1676; Conservative 0; Mismatches 417; Indels 54; Gaps 8;
QY 1 ATGTGTAAACCGAATTATGCGGCATGCTCTGTGGCCCTTACTTTTGGCATCTTGATC 60
Db 1 ATGTGTAAACCGAATTATGCGGCATGCTCTGTGGCCCTTACTTTTGGCATCTTGATC 60
QY 61 GCGCGCAATTTCGCGTGCAGCTGTGTGCAATCAACGCGCAGCGG----- 108
Db 61 GCGCGCAATTTCGCGTGCAGCTGTGTGCAATCAACGCGCAGCGGCTCTGCTCA 120
QY 109 TACCCGCTCACTTTCAAGCTAAGGACGTTCCCACTTGGCTCTGCGGCTCTTCGGTA 168
Db 121 GATTCCAAATCTTCCAAATCTTCGCGGATAAGCTCTGCTCAGCTCTGCGGAGCCTTCGGTA 180
QY 169 GAACACGCGGTCACACGACCGCGTGTGGTGGGCAATGCGGCTGTGTGAGACGGAAT 228
Db 181 GAAATACGCGGTCACACGCGCGCGCTGCTGCGCAATGCGGCTGCCAAGCGGAAT 240
QY 229 ATTGCAACTTCTGATAAGGATGCGCAATGATTTCCAAATGCAACAAACAGCAGAGAAAG 288
Db 241 ATCGCACTTTGATAAAATGGTAATGAAATTCCAATAGTAAGCAGCAGAGAGATAT 300
QY 289 CTGTCGTTTAAAGAGGAGATATCTGTTTATACGGTTCCAAAAAGATCAACGTCAG 348
Db 301 CTGCGCTTCAAGAGAGGATATCTGTTTATAGCGGTACGCCGAAAGAACAGGCTGAC 360
QY 349 CAGCTTAAAGATATAATTCGTCAACCAAAATCTTACGCGCAAGCATTTACCAATTCGAAAG 408
Db 361 AAATTTAAAGGAATCAACGCGGCTCTTAATGACCAATCTACAGCTCCGATTTA 420
QY 409 AAAAAATAAAAAATATGATTAATAATTTGTAGATGACAGGTTATGATATATCAACAGCA 468
Db 421 AAAGATGATGCGTATCAATATAAATATGTCCGGCGGATATGTTTATACATGATGGA 480
QY 469 AAAGATGAAATTTAGTGGAGTTCAAATTAACAGCAGTCTTACCAACCGGTTTGGTTATGAC 528

Db 481 ACAGATGAAATCGAAACAGAACTCAGGCGGTAAAGCGGTATCCACCGCTTAGGTTATGAC 540
QY 529 GGTTCCTGATATATTCGCGAGAACATCTTCGCAATCTTTTACCGAGCGGGAACGGTG 588
Db 541 GGTTCCTGATATATTCGCGAGAACGCTTCCTCCCAATCTTTTACCGAGTGGGGAACGGTG 600
QY 589 AAATATTCGCGCAACTGCGCAATATGACCGATGCCATACGTCATCGAACAGGAAAGCA 648
Db 601 GAATATTCGCTGTAATGCAATATGACCGATGCCAAACGTCATCGAGCAGGTGAGGC- 659
QY 649 GGAGATCTGAGCAAGATTTGGGTATATCTGTTTATACGCTCAAAATGTCGAGCAACT 708
Db 660 --GGTTGGCAATGCAATTTGGGTATATCACTTTTATGTTAAGCATGTTGTTGCACT 717
QY 709 TCTTATGCTGCGACTGCGCAGCAGCCGCGGAGGAGAAACATCTCTGCCAATATACGTTAAT 768
Db 718 TCTTATGCGCTTAGGATGTCGACGAAAGGAAAGCATCTCTGCCAATATACGTTGAT 777
QY 769 TTGACCAAAAAAATCTGAAATGGCAAGCTGATTAATAATCAGTATGTC- --AAAGAGA 825
Db 778 TTTGATAACAAAAACCATGAATGGCAAGCTGATTAATAATCAGTATGTCGAAATATAAAA 837
QY 826 GATGATCTTAAAAAACCACTGACCATTTACGACATTTACTGCAAAATTTGACGCGCAACCGC 885
Db 838 GATGAACCCAAAAACCGCTGACCATTTACGACATTTACTGCAAAATTTGACGCGCAACCGC 897
QY 886 TTTTACCGCAGTGCCAAAAAGTTAAACACAGAGGTGAAGACGAATCAGCTGATTAAGATAT 945
Db 898 TTTTACCGCAGTGCCAAAGTCAATCTGATTTAGCGAAAAACCTTCCCGGTATAGCGCT 957
QY 946 TTGTTTTTCCATACCGATCCGATCAGCGCTTAGGCGGCTTTTTCGCGATAGGGG 1005
Db 958 TTGTTTTTCCATGCGATCCGATCAGCGCTTAGGCGGCTTTTTCGCGATAGGGG 1017
QY 1006 GAAGAGCTTGCAGGACGGTTTATCAGCAACGACCAAGCAGCTATTCGCGCTGTTCGAGGC 1065
Db 1018 GAAGAGCTTGCAGGACGGTTTATCAGCAACGACCAAGCAGCTATTCGCGCTGTTCGAGGC 1077
QY 1066 AAACAAAAACAGACAGCAGCAACGCAATCAGATACAAATCTCTGCCCTGCGCTCTGAAAA 1125
Db 1078 A---AAACAAACAGACAGCAGCAACGCAATCAGATACAAATCTCTGCCCTGCGCTCTGAAAA 1134
QY 1126 CACACCAAAATCTTGGATCTCTAAAAATTTTCGTTGACGAGCAAGTGTGTGAAATATCC 1185
Db 1135 CACACCAAAATCTTGGATCTCTAAAAATTTTCGTTGACGAGGCACTGATGCGCATGCC 1194
QY 1186 CGACCGTTGAGGTTCCACTATGCGGATTTTGGTCTATCCGACAAACTTTTGTGAA 1245
Db 1195 CGTAAGTTTGCCTATTCCTCTATGCCCGATTTTGGTCTATCCGACAAACTTTTGTGAA 1254
QY 1246 GGGCTGCAAAATCTTCTTGTGTAACAAAGACAAACCAATCGATCTTGGCGAGCGGAGAA 1305
Db 1255 GGGCTGCAAAATCTTCTTGTGTAACAAAGACAAACCAATCGATCTTGGCGAGCGGAGAA 1314
QY 1306 ATGACCGTTCGCTGCTGTTGCGATTTTGGACCTATGTAACCTCGAGCGGATATAAAC 1365
Db 1315 ATGACCGTTCGCTGCTGTTGCGATTTTGGACCTATGTAACCTCGAGCGGATATAAAC 1374
QY 1366 GAACGCGCGCGCTTCCAAACGAGCGCAGGATCAAGAGGGGAGGAGAGAGGGGTGATGAC 1425
Db 1375 GATCGCGCGCAAGTAACCAAGCGGAGATTAAGGGGAGGATGAAGAGGGTGCAGGC 1434
QY 1426 GTTGATACCGTGAAGAAAGCAAGACGAAATCGGCGATGAAGAAAGCACCGGAGACGAA 1485
Db 1435 GTTGATACCGAGAGAAAGCAAGACGAAAGCGGTAGAGAGGATGAAGAGGGTGCAGGC 1494
QY 1486 G-----TCGTGAGAGATGAAGACGAAATGAGN-----CGAAGAGAAATCGAA 1530
Db 1495 GAAACTTCGAAAGAGGATATGCGGAGACGAAAGCAACCGCGAGAGAAACCGAA 1554
QY 1531 GAAGACCTGAGAGAGAGCTGAAGAGGAAAGACCGGAGAGAAATTTCCCGCAGAGAA 1590

Db 1555 GAAGTTGATGAAGCGAAGAGGAGAGTTCGAAGAACCCGAGAAATATCGCCGCGAGAA 1614
Qy 1591 GGCAACGCGCGTTTCAGGAGCATCTGCGCACTCGGAGAGCTCTAAGAGGAGGAGCATC 1650
Db 1615 GGCAACGCGCGTTTCAGGAGCATCTGCGCGCTCTAGAGGAGCTCTAAGAGGAGGAGCATC 1674
Qy 1651 GACCTTTCTGAAAGGTATCCGACGCGCGAAGCGGACATTCCTCAAAAAAGCGAAGCGG 1710
Db 1675 GACCTTTCTGAAAGGTATCCGACGCGGAGAGAGATATCCGAAAGCGGAGCGG 1734
Qy 1711 CATATACCGGCACTTCGGAGCGGTATCGGCGATATCGGATAGTGGTACGTCCATTCAA 1770
Db 1735 CATATACCGGCACTTCGGAGCGGTATCGGC-----AAACCAATTCAA 1779
Qy 1771 AAGGATAGCTATCGCAAT---CAAGGGGCAAAAGCAGAAATTTACCGTTGATTTGAAAGCG 1827
Db 1780 TGGGACAAATCAGCGGAGTGAAGAGCGGCAAGAGCAATTTACCGTTGATTTGCAAG 1839
Qy 1828 AAGAGGTGTCGGAAATGCTTGACAGAAAAAATGATACAAACCCCGCTTTTATATGAA 1887
Db 1840 AATCGATTTCCGAAAGCTGACGGAGCAAAACGCGGTAGAACCTGCTTTCCATATGAA 1899
Qy 1888 AAGAGGTGATGACAGGTAAAGGTTTCCAGCTTTTGGCGATATCGGAGAACGATTT 1947
Db 1900 GACGGCAAGATTTATGGCAACGGTTTCCAGCGACAGCGGCACCTCGGAGAGCGGCATC 1959
Qy 1948 GACCTTTCTGGGAGCGGTTCGACTAACCCGAGAACTTCAAGCAACCCCGCTTTTATATGAA 2007
Db 1960 AATCTTTCCGAAATGTTGACCGGACCCCAAAACATTCGAAGCTAGTAACTCTTGTA 2019
Qy 2008 ACAGGGCGTTTATGGCCCGGAGCGGAGAAATTTGGGCGGTAAATATTCAGACGAG 2067
Db 2020 GAAGAGGATTTTACGGCCCGGAGCGCGGAAATTTGGGCGGTACTATTTTCAATATGAT 2079
Qy 2068 CGGAAATTCGGTGGTATTTGGGCGGAAAAAAGATGACAGAGGC 2114
Db 2080 GGGAAATCTCTTAGTATACTGAAATATTTGAAATGAACTGAAAGC 2126

RESULT 7

US-10-343-561-15
; Sequence 15, Application US/10343561
; Publication No. US20040126389A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Dalemans, Wilfried
; APPLICANT: Denoel, Philippe
; APPLICANT: Dequesne, Guy
; APPLICANT: Feiron, Christiane
; APPLICANT: Garcon, Nathalie
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Thiry, Georges
; APPLICANT: Thonnard, Joelle
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: Vaccines Comprising Outer Membrane
; TITLE OF INVENTION: Vesicles from Gram Negative Bacteria
; FILE REFERENCE: B45260
; CURRENT APPLICATION NUMBER: US/10/343,561
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/EP01/08857
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: EP 00956369.3
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: GB 0103170.7
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-343-561-15

Query Match 23.4%; Score 497.6; DB 17; Length 1000;
Best Local Similarity 75.8%; Pred. No. 8.2e-118;
Matches 679; Conservative 0; Mismatches 189; Indels 28; Gaps 4;
Qy 1213 GATTTTGGTTCATCCCGACAAACTTTCTTGTCTGAAGGGCGTGAATTTCTTTGGTGAACAAA 1272
Db 1 GATTTTGGTTCATCCCGACAAAGCTTTCTTGTCTGAAGGGCGTGAATTTCTTTGGTGAACAAA 60
Qy 1273 GAACAAACCAATCGATCTTTGCGGACGGCAGGAAATGACCGTCTTGTTCGACATTT 1332
Db 61 GAGAAACCAATCAAGCTTGCCTGATGCGAGGAAATGACCGTCTTGTTCGACATTT 120
Qy 1333 TTGACCTATCTGAAACTTCGACGAGTAAACCGAACCGCCCGCGTCCAAACGGAAGCG 1392
Db 121 TTGACCTATCTGAAACTTCGACGAGTAAACCGAACCGCCCGCGTCCAAACGGAAGCG 180
Qy 1393 CAGGATGAAGAGGGGACCGAAGAGGGTGTAGGCGTTGATACCGTAAAGAAAGCGAGAC 1452
Db 181 GAAGATAAAAGGAGGATGAAGAGAGTGCAGGCGTTGTAACTCGAAGAGCGGAGGC 240
Qy 1453 GAAATCGGCGATCAACAAAGCACCAGAGAGAGTCTGTAAGATGAAGACGGAAGTAA 1512
Db 241 GAGATTTCCGAAAGTGA-----AGCGAAGAAAGCGGAAATCTGCGAAGAA 291
Qy 1513 GACGAAGAAATCGAAGAAACCTGAAGAGAGCTGAAGAGGAGAACCCCGAAGAA 1572
Db 292 CCGGAAGAGAGCTGAAGAGAGAGAGCTGAACCCAAAGAGTTGAAGAAACCGAAGAA 351
Qy 1573 GAAATTCGCGGAGAGAGAGGCAACCGCGGTTTCAGGAGCATCTTGCCTCCTCGGAGGC 1632
Db 352 AATTCGCGGAGAGAGAGGCAACCGCGGTTTCAGGAGCATCTTGCCTCCTCGGAGGC 411
Qy 1633 TCTAAGGAGGAGGAGCATGACCTTTTCTGAAAGGTATCCGACGCGGAGCGGATTCGGAT 1692
Db 412 TCTAAGGAGGAGGAGCATGACCTTTTCTGAAAGGTATCCGACGCGGAGCGGATTCGGAT 471
Qy 1693 CCAAAAAACGGAACGCGCATTTATACCGGCACTTACCGGCACTTGGGAAAGCGGATTCGGAT 1752
Db 472 CCAAGAACCGGAAAGGAGCACTTATACCGGCACTTGGGAAAGCGGATTCGGATTCGGAT 522
Qy 1753 AGTGATAGTCCATTTCAAAAGGATAGTATGCG---AATCAAGGGGCAAAAGCAGAAATTT 1809
Db 523 -----ACACCCANTCAATGGGCAATCAGCGGAGTAAAGAGCGGCAAAAGCAGAAATTT 576
Qy 1810 ACCGTTGATTCGAGGAGGAGGAGCGGTTCGGAATGCTGACAGAAAAAATGATACAC 1869
Db 577 ACCGTTAATTTCCGCGAGAAATCGATTTCCGGAACGCTGACGAGAAAAACGCTGTACAA 636
Qy 1870 CCGCTTTTATATTTGAAAAAGGTGATGATGACGTAACCGTTTCCAGCGTTTGGCGGAT 1929
Db 637 CCGCTTTTATATTTGAAAAAGGTGATGATGACGTAACCGTTTCCAGCGTTTGGCGGAT 696
Qy 1930 ACTCGGAGAAACGATATTTGACCTTTCTGGGAGCGGTTTCCGTAACCCGAAAGCTTCAAA 1989
Db 697 ACTCGTGAAGACGATCAATCTTTCCGGAATGTTTCCGTAACCCGAAAGCTTCAAA 756
Qy 1990 GCGGACATCTTCTTGAACAGCGGCTTTTATGGCCCGGAGCGGAGAAATTTGGCGGT 2049
Db 757 GCTAGTATCTTCTGTTAGAGGAGGATTTTACGCGCGCA-CGCGAGGAAATTTGGCGGT 815
Qy 2050 AATATTTATGACAGCAGCGGAAATTCGGTGGGATTTGGGCGGAAAAAGATGA 2105
Db 816 AATATTTCAATGAAGATGCGGAAATCTTTGGTATTAAGTGAAGTACTGAAAAATA 871

RESULT 8

US-10-467-534-80
; Sequence 80, Application US/10467534
; Publication No. US20040131625A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves

Matches	141; Conservative	07; Moderate	01; Relaxed
QY	1394	AGGATGAGAGGGGGACGAGAGGGTGTAGGCGTTGATACGGTAAAGAAACGGAGACG	1453
Db	366742	AAGAGGAAGAGGAAGAGAGAGAGGAAGAGGAGAGAGAGGAAGAGGAGAGAGAG	366583
QY	1454	AAATCGCGGTGATGAGAGAGACACCGAGACGAAGTCGTAGAAAGATGAAGACGAAGATGAAG	1513

US-10-087-192-463

18378 AAGAAGAAGAAGAAG 18361

; CURRENT FILING DATE: 09/07/2009
; PRIOR APPLICATION NUMBER: US 09/747,377

;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: US 09/798,586
;; PRIOR FILING DATE: 2001-03-02
;; NUMBER OF SEQ ID NOS: 2059
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 49
;; LENGTH: 37265
;; TYPE: DNA
;; ORGANISM: Mus musculus
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(37265)
;; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-49

Query Match
Best Local Similarity 4.5%; Score 96.6; DB 13; Length 37265;
Matches 138; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1394 AGGATGAAGAGGGGACGAGAGGGTGTAGCGCTTGATACGGTAAAGAAAGCGAGACG 1453
Db 29840 AAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 29899

QY 1454 AATCGCGGATGAAGAAAGCAGCGGAGACGAAGTCTGTAGAGATGAAGACGAAGATGAAG 1513
Db 29900 AAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 29959

QY 1514 ACCAAGAGAAATCGAAGAGAGACCTGAGAGAGAGCTGAGAGAGAGAGACCGCGAAGAG 1573
Db 29960 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 30019

QY 1574 AATGCGCGGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1600
Db 30020 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 30046

RESULT 12

US-10-322-281-773/c
; Sequence 773, Application US/1032281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 115223
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(115223)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-773

Query Match
Best Local Similarity 4.5%; Score 96; DB 17; Length 115223;
Matches 150; Conservative 0; Mismatches 308; Indels 0; Gaps 0;

QY 1165 GAGCAAGTGTGAAATCCCGACCGTTTGAGGTTTCCATATGCCCGATTTTGGTCAT 1224
Db 9462 GAGGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 9403

QY 1225 CCGACAAACTTCTTGTGCGAGGCGTGAAATTCCTTTGTTAACAAGACAAACCATC 1284
Db 9402 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 9343

QY 1285 GATCTTCCGACGAGGAAATGACCGTCGCTGCTTTGTCGACTTTTGTGACCTATGTG 1344

Db 9342 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 9283
QY 1345 AAACCTCGGACGATAFAAAACCGAACGCCCGCCCTCAACCGAAGGCCGACGATGAAGAG 1404
Db 9282 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 9223
QY 1405 GGGGACGAAGAGGGTGTAGCGCTTGATACCGTAAAGAAAGCGAAGACGAAATCGCGAT 1464
Db 9222 GGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9163
QY 1465 GAAGAAAGCACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1524
Db 9162 GGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9103
QY 1525 ATCGAAGAGAACTCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1584
Db 9102 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9043
QY 1585 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1622
Db 9042 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9005

RESULT 13

US-10-027-632-269927/c
; Sequence 269927, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269927
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-269927

Query Match
Best Local Similarity 4.5%; Score 95.4; DB 13; Length 635;
Matches 135; Conservative 1; Mismatches 67; Indels 0; Gaps 0;

QY 1388 AGCGCAGGATGAAGAGGGGACGAGAGGGGTGTAGCGCTTGATACCGTAAAGAGAGCG 1447
Db 425 ACGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366

QY 1448 AAGACGAATTCGGCGTGAAGAAAGCAACCGAGACGAAGTCGTAGAGATGAAGACGAAG 1507
Db 365 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306

QY 1508 ATCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1567
Db 305 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246

QY 1568 AAGAAGATTTGCCGCGAGAGAGAA 1590

Qy 1569 AGAAGAATTGCCGCGAGAAGAAGCAAG 1597
| | | | |
Db 43 AGAAGAAGAAGAAGAAGAAAATTAAAG 15

Search completed: August 25, 2004, 14:58:25
Job time : 1076.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 4846.67 Seconds
(without alignments)
13086.780 Million cell updates/sec

Title: US-10-735-098-9
Perfect score: 2124
Sequence: 1 atgtgtaaacggaattatgg.....acaaggaggcaacacgatga 2124

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	103.4	4.9	531	14	CD915362
2	101	4.8	802	28	BH066160
C 3	100.8	4.7	434	14	CA745444
C 4	99.4	4.7	289	14	CA716220

5	99.2	4.7	223	13	CA022136
6	99	4.7	395	29	CE760553
7	98.8	4.7	264	13	BQ241566
8	98.6	4.6	729	29	CE180020
C 9	98.6	4.6	1096	14	CK206118
10	97.6	4.6	799	28	BZ201507
11	97.4	4.6	575	10	BF707975
C 12	97.2	4.6	232	29	CG321416
C 13	97.2	4.6	233	12	B7454017
C 14	97.2	4.6	691	28	BH040136
15	97	4.6	675	28	BZ104011
16	96.8	4.6	278	13	BQ460618
17	96.8	4.6	744	28	BH065422
C 18	96.8	4.6	774	28	AZ658872
19	96.6	4.5	477	14	CD111846
20	96.6	4.5	960	28	CC143364
C 21	96.4	4.5	263	13	BU005139
22	96.2	4.5	719	28	BH360392
C 23	95.8	4.5	311	14	CA699402
24	95.8	4.5	980	13	BU944408
25	95.6	4.5	332	14	CA566759
C 26	95.6	4.5	605	28	BZ222147
27	95.6	4.5	617	14	CA743799
28	95.4	4.5	205	13	BQ241058
C 29	95.4	4.5	546	28	AZ600777
30	94.8	4.5	341	29	CE510654
31	94.6	4.5	924	13	BQ925195
32	94.2	4.4	340	13	BQ462203
C 33	94	4.4	483	28	AZ060017
34	94	4.4	527	28	AZ279446
35	94	4.4	596	29	CG660549
C 36	93.8	4.4	613	29	CE357285
C 37	93.8	4.4	880	28	AZ529191
38	93.8	4.4	953	13	BQ939407
39	93.6	4.4	293	13	BQ459561
40	93.6	4.4	295	13	BU976670
41	93.6	4.4	665	13	BU432980
42	93	4.4	342	11	AY383662
43	93	4.4	537	14	CF380795
44	92.8	4.4	358	28	AZ582992
45	92.8	4.4	495	14	CD663452

ALIGNMENTS

RESULT 1
CD915362

LOCUS
DEFINITION

CD915362
G550.125001F010713 G550 Triticum aestivum cDNA clone G550125001,
mRNA sequence.

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae;

Spermatophyta; Magnoliophyta;

Poideae; Triticeae; Triticum.

1 (bases 1 to 531)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>)

and <http://genoplante-info.infobiogen.fr>.

Location/Qualifiers

source

1. .531

/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G550125001"
/tissue_type="grain (550 degrees per day after
pollination)"
/clone_lib="G550"

ORIGIN

Query Match 4.9%; Score 103.4; DB 14; Length 531;
Best Local Similarity 67.3%; Pred. No. 2.7e-10;
Matches 146; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1396 GATGAAGAGGGGCGACCAAGAGGGTGTAGCGCTTGATACGGTAAAGAAAGCGAAGCAGAA 1455
DB 22 GAGGAAGAGGAAGAGAGAGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 81
QY 1456 ATCGCGGATGAAGAAAGCACCAGAGAGAGTCTGTAGATGAAGATGAAGATGAAGAC 1515
DB 82 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 141
QY 1516 GAAGAGAGATCGAGAGAGAACCTGAAGAGAGAGCTGAAGAGAGAGAACCCGAAGAGAA 1575
DB 142 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 201
QY 1576 TTGCGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1612
DB 202 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 238

RESULT 2

BH066160
LOCUS RPCI-24-285J5.TJ RPCI-24 802 bp DNA linear GSS 18-JUL-2001
DEFINITION RPCI-24-285J5.TJ RPCI-24 Mus musculus genomic clone RPCI-24-285J5,
genomic survey sequence.

ACCESSION BH066160

VERSION BH066160.1 GI:14884017

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 802)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,
Russell, D., de Jong, P., and Fraser, C.M.

REFERENCE Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

CONTACT: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 285 row: J column: 5

Seq primer: SP6

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..802

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-24-285J5"

/sex="Male"

/cell_type="Spleen/Brain"

/clone_lib="RPCI-24"
/note="vector; PTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the PTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN

Query Match 4.8%; Score 101; DB 28; Length 802;
Best Local Similarity 65.1%; Pred. No. 8.3e-10;
Matches 149; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1387 AAGCGCAGGATGAAGAGGGGCGACCAAGAGGGTGTAGCGCTTGATACGGTAAAGAAAGC 1445
DB 324 AATTCGAAAAAGTAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 383
QY 1447 GAAGACGAATTCGGCGATGAAGAAAGCACCAGAGAGAGTCTGTAGAGATGAAGACGAA 1506
DB 384 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 443
QY 1507 GATGAAGACGAAGAGAAATCGAAGAGAAACCTGAAGAGAGAGCTGAAGAGAGAGAACCC 1566
DB 444 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 503
QY 1567 GAAGAAGAGATTCGCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
DB 504 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 552

RESULT 3

CA745444/c

LOCUS CA745444

DEFINITION CA745444.1 GI:25561267

ACCESSION CA745444

VERSION CA745444.1

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

1 (bases 1 to 434)

Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.

REFERENCE Dupont Wheat cDNA Sequence

Unpublished (2002)

CONTACT: Scott V. Tingey

Crop Genetics

E. I. Dupont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: T7.

Location/Qualifiers

1..434

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone="wri2s.pk001.i6"

/tissue_type="leaf"

/lab_host="DH10B"

/clone_lib="wri2s"

/note="vector; PCGM-T Easy; Site 1: SmaI; Riband
(susceptible) wheat leaves infected with Septoria tritici
strain A, 48 hours after infection, subtracted w/
comparable uninfected leaves"

ORIGIN

Query Match 4.7%; Score 100.8; DB 14; Length 434;
Best Local Similarity 67.1%; Pred. No. 8.9e-10;
Matches 141; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy	1382	AACCGAGGCGCAGGATGAAGAGGGGGACGAAGAGGGTGTAGGCGTTGATAACCGTTAAG	1441
Db	381	AACTGGAGAGCGAAGACGAGGAGGAGGAAGAAGAGAGNNGAGGACGACGAGGAGG	322
Qy	1442	AAACCGAAGACGCAATTCGCCATCGAAGAACCCGGAGACGAAGTCGTAGAAGATCAAG	1501
Db	321	ARGNAGAGAGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	262
Qy	1502	ACGHAGATGAAGACGAAGAAGAAATCCAAGAAGAACCTGAAGAGAGAGCTTGACGAGGAAG	1561
Db	261	AAGAAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	202
Qy	1562	AACCCGAAGAAGAAATTCGCCGCGAGGAAG	1591
Db	201	ARGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	172

RESULT 4
CA716220/c
LOCUS
DEFINITION
 289 bp mRNA linear EST 26-NOV-2002
wdk3c.pk024.i22 wdk3c Triticum aestivum cDNA clone wdk3c.pk024.i22
5' end, mRNA sequence.
CA716220
CA716220.1 GI:25438013
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 289)
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com

```

FEATURES
seq primer: M13.
Location/Qualifiers
1. .289
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wdk3c.pk024.i22"
/tissue_type="kernel"
/lab_host="DHI08"
/clone_lib="wdk3c"
/notes="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum L.) developing kernel, 14
days after anthesis."

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Query Match 4.7%; Score 99.4; DB 14; Length 289;
Best Local Similarity 67.5%; Pred. No. 1.7e-09;
Matches 139; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

[illegible]

QY	1566	GGAAGAAGAAATGTCGGCAGAGAAG	1591
Dd	72	AGAGAAGAAGAAGAAGAAG	47
RESULT 5			
CA022136			
LOCUS	H542E07r	HZ Hordeum vulgare subsp. vulgare	223 bp mRNA linear EST 23-OCT-2002
DEFINITION	5-PRIME,	MRNA sequence.	
ACCESSION	CA022136		
VERSION	CA022136.1	GI:24299510	
KEYWORDS	EST.		
SOURCE	Hordeum vulgare subsp. vulgare		
ORGANISM	Hordeum vulgare subsp. vulgare		
	Eukaryota; Viridiplantae;		
	Spermatophyta; Magnoliopsida; Poales;		
	Poaceae;		
	Pooideae; Triticeae; Hordeum.		
	1 (bases 1 to 223)		
REFERENCE	Radchuk,V., Zhang,H., Weschke,W., Potokina,E. and Wobus,U.		
AUTHORS	Barley ESTs from developing seeds		
TITLE	Unpublished (2002)		
JOURNAL	Contact: Stein Nils		
COMMENT	Molecular Markers Group, Department Genbank		
	Institute of Plant Genetics and Crop Plant Research (IPK)		
	Cornrestr. 3, 06466, Gatersleben, Germany		
	Tel: 039482-5522		
	Fax: 039482-5595		
	Email: stein@ipk-gatersleben.de		
	Insert Length: 223 Std Error: 0.00		
	Plate: 42 row: E column: 7		
	Seq primer: ML3rev.		

FEATURES	source
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source
1. .223
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:275541"
/db_xref="taxon:112509"
/clone="HZ42E07"
/tissue_type="pericarp"
/dev_stage="0-7 DAP (days after pollination)"
/lab_host="Xil10-Gold"
/clone_lib="HZ"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); pericarp 0-7 DAP(days after pollination). Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable.Average insert size is 900 bp"

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ORIGIN

```

Query Match      4.7%; Score 99.2; DB 13; Length 223;
Best Local Similarity 67.3%; Pred. No. 1.8e-09;
Matches 140; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```

[illegible]

QY 1564 CCCGAGAGAGAAATTGCGCGGAGAGAG 1591
Db 181 GACGAGAGAGAGAGAGAGAGAGAGAG 208

RESULT 6
CE760553
LOCUS
DEFINITION tigr-gss-dog-17000369997532 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE760553
VERSION CE760553.1 GI:37101172
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 395)
AUTHORS Kirkness,E.F., Baina,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
MEDLINE Science 301 (5641), 1898-1903 (2003)
PUBMED 22875432
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source
1..395
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 4.7%; Score 99; DB 29; Length 395;
Best Local Similarity 62.2%; Pred. No. 2e-09;
Matches 156; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 1357 ATAAAACCGAACGCCCGCCGTCCTCAACCGAGCGCGGATGAAGAGGGGAGAGAG 1416
Db 58 AGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 117
QY 1417 GGTGTAGGCGTTGATACGCTGTAAGAAAGCGAAGACGAAATCGCGATGAAGAAAGCACC 1476
Db 118 GGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 177
QY 1477 GGAGACGAGAGTCTGTAGAGATGAAGACGAGATGAAGACGAGAGAAATCGAAGAGAA 1536
Db 178 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 237
QY 1537 CCTGAAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1596
Db 238 GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
QY 1597 GGCGGTTTCAGG 1607
Db 298 GAAGAGAGAGG 308

RESULT 7
BQ241566
LOCUS
DEFINITION TaE05003E07R TaE05 Triticum aestivum cDNA clone TaE05003E07R, mRNA

sequence.
BQ241566
BQ241566.1 GI:20437442
EST.
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 264)
AUTHORS Cloutier,S.
TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@agr.gc.ca
Was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 003 row: E column: 07
Seq primer: M13 Reverse.
Location/Qualifiers
1..264
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TaE05003E07R"
/tissue type="developing seeds"
/dev stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/clone_lib="TaE05"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site 1:
NotI; Site 2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"

ORIGIN
Query Match 4.7%; Score 98.8; DB 13; Length 264;
Best Local Similarity 68.7%; Pred. No. 2.2e-09;
Matches 136; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 1394 AGGATGAAGAGGGGAGAGAGAGGCTGTAGCGCTTGATACGCTAAAGAAAGCGAAGC 1453
Db 43 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 102
QY 1454 AATCGCGGATGAAGAAAGCAGCGAGAGCGAGTCGTAGAGATGAAGACGAGATGAAG 1513
Db 103 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 162
QY 1514 ACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1573
Db 163 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
QY 1574 AATTGCCGCGAGAGAGAG 1591
Db 223 AAGAAGAGAGAGAGAGAG 240

RESULT 8
CE180020
LOCUS
DEFINITION tigr-gss-dog-17000326768259 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE180020
VERSION CE180020.1 GI:35328914
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

1 (bases 1 to 729)
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432
 MEDLINE
 PUBMED
 14512627
 COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

source
 Location/Qualifiers
 1..729
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /notes="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 4.6%; Score 98.6; DB 29; Length 729;
 Best Local Similarity 67.8%; Pred. No. 2.5e-09;
 Matches 140; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
 QY 1386 GAAGCGCAGGATGAGAGGGGACGAGAGGGGTGAGCGTGTGTAACGTTAAGAAAG 1445
 DB 168 GAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227
 QY 1446 CGAAGCAGAAATCGGCGATGAGAGAAAGCCGCGAGACGAGTGGTGAAGAGATCAAGACCA 1505
 DB 228 AGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 287
 QY 1506 AGATCAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1565
 DB 288 AGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 347
 QY 1566 CGAAGAAGATTCGCGCGCAGAGAGAGGCA 1594
 DB 348 AGAAGAAGATTAGGATCAAAATATGCA 376

RESULT 9

CK206118/c
 LOCUS
 DEFINITION FGAS017695 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
 aestivum cDNA, mRNA sequence.
 ACCESSION CK206118
 VERSION CK206118.1 GI:39568508
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE

1 (bases 1 to 1096)
 Allard, F., Crosby, W.L., Danyluk, J., Eudes, P., Frick, M., Gaudet, D.,
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
 Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
 Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops
 Unpublished (2003)
 COMMENT
 Contact: Wm L Crosby
 Bioinformatics
 University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_est@cs.usask.ca

This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [29 696].

Plate: L5B006 Row: F Column: 12.

FEATURES

source
 Location/Qualifiers
 1..1096
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"

/notes="Vector: PCMV.SPORT6; Crown and developmental stages
 of spike formation in wheat cultivar Norstar. 4 mRNA
 populations were combined before constructing the library.
 The first mRNA population is from 1cm crown sections after
 30 days of cold acclimation. The second is from 1cm crown
 sections after 11 days of deacclimation (before
 deacclimation plants were fully vernalized for 49 days).
 The third is from different developmental stages of spike
 formation (5 to 50mm) that still have not emerged from the
 leaf (dissection required). The last is from different
 developmental stages of spike and seed formation after
 having emerged from the leaf (visible). First strand
 synthesis in this library was done in the presence of
 methylated dCTP thereby protecting from internal cleavage
 with NotI."

ORIGIN

Query Match 4.6%; Score 98.6; DB 14; Length 1096;
 Best Local Similarity 63.9%; Pred. No. 2.6e-09;
 Matches 149; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 1359 AAAAACCGAACCCCGCGTCCAAACCGAAGCGCAGGATGAGAGGGGAGAGAGGG 1418
 DB 300 AGAACCAAGAGACCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 241
 QY 1419 TGTAGCGTTGTATACGTTAAAGAAAGCGAAGACGAAATTCGGCGATGAAGAAAGCACC 1478
 DB 240 AGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
 QY 1479 AGACGAAGTCTGTAGAGATGAGACGAGATGAGACGAGAGAAATTCGAGAGAGAAC 1538
 DB 180 AGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
 QY 1539 TGAAGAAGAGCTGAAGAGAGAGAACCCGAGAGAGAAATTCGGCGCAGAGAGAG 1591
 DB 120 AGGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68

RESULT 10

BZ201507
 LOCUS
 DEFINITION BZ201507 799 bp DNA linear GSS 11-OCT-2002
 CH230-445016 TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
 CH230-445016, genomic survey sequence.
 ACCESSION BZ201507
 VERSION BZ201507.1 GI:23859559
 KEYWORDS GSS.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE

1 (bases 1 to 799)
 Zhao, S., Shetty, J., Shatsman, S., Tsengaye, G., Geer, K.,
 Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
 Riggs, F., de Jong, P. and Fraser, C.M.
 Rat BAC End Sequences from Library CHORI-230 MboI segment
 Unpublished (1999)
 Other_GSSs: CH230-445016.TV


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/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCK-; site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match          4.6%; Score 97.2; DB 29; Length 232;
Best Local Similarity 68.2%; Pred. No. 4.5e-09;
Matches 135; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1394 AGGATGAAGAGGGGACGAGAGGGTGTAGCGTTGATACGGTAAAGAAAGCGAAGC 1453
Db 214 AAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 155

QY 1454 AAATCGCGATGAAGAAAGCACCAGACGAGTCTGTAGAGATGACAGCAAGATGAAG 1513
Db 154 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 95

QY 1514 ACGAAGAGAAATCGAAGAGAACTCGAAGAGAGCTGAAGAGAGAGAGAGAGAGAGAG 1573
Db 94 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 35

QY 1574 AATTGCCGCGAGAGAGAG 1591
Db 34 AAGAAGAGAGAGAGAGAG 17

RESULT 13
BJ454017/c
LOCUS
DEFINITION
233 bp mRNA linear EST 23-MAY-2002
BJ454017 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak45j15 5', mRNA sequence.
ACCESSION
BJ454017
VERSION
BJ454017.1 GI:21132592
KEYWORDS
EST
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Eukaryota; Viridiplantae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 233)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
Location/Qualifiers
1..233
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baak45j15"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"

ORIGIN
Query Match          4.6%; Score 97.2; DB 12; Length 233;
Best Local Similarity 68.2%; Pred. No. 4.5e-09;
Matches 135; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1394 AGGATGAAGAGGGGACGAGAGGGTGTAGCGTTGATACGGTAAAGAAAGCGAAGC 1453
Db 201 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 142

```

```

QY 1454 AAATCGCGATGAAGAAAGCACCAGACGAGTCTGTAGAGATGACAGCAAGATGAAG 1513
Db 141 AGGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 82

QY 1514 ACGAAGAGAAATCGAAGAGAACTCGAAGAGAGCTGAAGAGAGAGAGAGAGAGAGAG 1573
Db 81 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 22

QY 1574 AATTGCCGCGAGAGAGAG 1591
Db 21 AACAAGAACGAGAGAGAG 4

RESULT 14
BH040136/c
LOCUS
DEFINITION
691 bp DNA linear GSS 17-JUL-2001
RPCI-24-255A23-TV RPCI-24 Mus musculus genomic clone
RPCI-24-255A23, genomic survey sequence.
ACCESSION
BH040136
VERSION
BH040136.1 GI:14818806
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 691)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-255A23.TU
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.choi.org/bacpac/orderingframe.html). BAC end
page: http://www.tigr.org/cdb/bac\_ends/mouse/bac\_end\_intro.html
Plate: 255 row: A column: 23
Seq primer: 17
Class: BAC ends.
FEATURES
Location/Qualifiers
1..691
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-255A23"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."
ORIGIN
Query Match          4.6%; Score 97.2; DB 28; Length 691;
Best Local Similarity 68.2%; Pred. No. 4.8e-09;
Matches 135; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1394 AGGATGAAGAGGGGACGAGAGGGTGTAGCGTTGATACGGTAAAGAAAGCGAAGC 1453
Db 475 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416

QY 1454 AAATCGCGATGAAGAAAGCACCAGACGAGTCTGTAGAGATGACAGCAAGATGAAG 1513

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